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OM protein - protein search, using sw model

Run on: August 9, 2006, 16:22:32 ; Search time 51 Seconds
(without alignments)
1084.693 Million cell updates/sec

Title: US-09-881-736A-2

Perfect score: 3243

Sequence: 1 MDTMMLNVRNLFEQLVRRVE.....SKSATNLGRQGNFFASPMLK 632

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*

- 1: /EMC Celerra_SIDS3/ptodata/2/iaa/5_COMB.pdp.*
- 2: /EMC Celerra_SIDS3/ptodata/2/iaa/6_COMB.pdp.*
- 3: /EMC Celerra_SIDS3/ptodata/2/iaa/7_COMB.pdp.*
- 4: /EMC Celerra_SIDS3/ptodata/2/iaa/H_COMB.pdp.*
- 5: /EMC Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pdp.*
- 6: /EMC Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pdp.*
- 7: /EMC Celerra_SIDS3/ptodata/2/iaa/backfiles1.pdp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3243	100.0	632	2	US-09-949-016-6844
2	1133	34.9	245	2	US-09-949-016-7193
3	301	9.3	1261	2	US-09-080-855-2
4	301	9.3	1261	2	US-09-566-076-2
5	282	8.7	838	2	US-09-949-016-9916
6	282	8.7	838	2	US-09-949-016-9917
7	281.5	8.7	1287	2	US-09-949-016-11527
8	278.5	8.6	1227	2	US-09-949-016-7008
9	270.5	8.3	2548	2	US-09-172-422-1
10	260.5	8.0	802	2	US-09-949-016-6235
11	257.5	7.9	185	5	PCT-US93-03076-10
12	255	7.9	589	2	US-10-094-749-1841
13	254.5	7.8	748	2	US-10-104-047-2336
14	254	7.8	750	2	US-09-949-016-11166
15	251	7.7	170	2	US-10-080-960-32
16	247	7.6	816	2	US-10-104-047-2328
17	238.5	7.4	761	2	US-09-949-016-8473
18	238.5	7.4	761	2	US-09-949-016-8474
19	238.5	7.4	761	2	US-09-949-016-8475
20	238.5	7.4	761	2	US-09-949-016-8476
21	237	7.3	601	2	US-09-949-016-8477
22	237	7.3	732	2	US-09-949-016-8478
23	237	7.3	732	2	US-09-949-016-8479
24	237	7.3	836	2	US-09-949-016-11057
25	237	7.3	836	2	US-09-949-016-11058
26	237	7.3	836	2	US-09-949-016-11059

RESULT 1

US-09-949-016-6844

; Sequence 6844, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 6844

; LENGTH: 632

; TYPE: PRT

; ORGANISM: Human

; US-09-949-016-6844

Query Match 100.0%; Score 3243; DB 2; Length 632;
Best Local Similarity 100.0%; Pred. No. 2e-298;
Matches 632; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDTMMLNVRNLFEQLVRRVEILSEGNEVQFIOLAKDFEDFRKKWQRTDHELKGYKDLLMK 60

DB 1 MDTMMLNVRNLFEQLVRRVEILSEGNEVQFIOLAKDFEDFRKKWQRTDHELKGYKDLLMK 60

QY 61 ATERSALDVKLKHARNQVDVEIKRQRAEADCEKLERQIOLIREMLMCDTSGSIQLSSE 120

DB 61 ATERSALDVKLKHARNQVDVEIKRQRAEADCEKLERQIOLIREMLMCDTSGSIQLSSE 120

QY 121 QKSALAFNLNRGQPSSSNAGNKLSTIDSGSILSDISFDKTDSDSLDWSLVTFKLKKR 180

DB 121 QKSALAFNLNRGQPSSSNAGNKLSTIDSGSILSDISFDKTDSDSLDWSLVTFKLKKR 180

QY 181 EKRRSTSRQFVDGPPGPKVKTRSIGSAVDQGNESIVAKTIVTVPNDDGGPIEAVSTIETVP 240

DB 181 EKRRSTSRQFVDGPPGPKVKTRSIGSAVDQGNESIVAKTIVTVPNDDGGPIEAVSTIETVP 240

QY 241 YWTRRRRTGTTLQPNWSDTLNSRQLEPRTEVDSVGTTPQSGMRHLHDFVSKTVIKPESC 300

DB 241 YWTRRRRTGTTLQPNWSDTLNSRQLEPRTEVDSVGTTPQSGMRHLHDFVSKTVIKPESC 300

ALIGNMENTS

27 237 7.3 836 2 US-09-949-016-11060 Sequence 11060, A
28 237 7.3 1045 2 US-09-949-016-8469 Sequence 8469, Ap
29 237 7.3 1045 2 US-09-949-016-8470 Sequence 8470, Ap
30 237 7.3 1045 2 US-09-949-016-8471 Sequence 8471, Ap
31 237 7.3 1045 2 US-09-949-016-8472 Sequence 8472, Ap
32 230 7.1 140 5 PCT-US93-03076-9 Sequence 9, Appli
33 229.5 7.1 655 2 US-09-949-016-6759 Sequence 6759, Ap
34 229.5 7.1 669 2 US-09-949-016-10241 Sequence 10241, A
35 225.5 7.0 420 2 US-10-094-749-3217 Sequence 3217, Ap
36 218 6.7 103 2 US-10-080-960-34 Sequence 34, Appl
37 214.5 6.6 547 2 US-09-855-323-15 Sequence 15, Appl
38 210 6.5 1513 5 PCT-US93-03076-2 Sequence 2, Appli
39 205.5 6.3 763 2 US-09-949-016-10382 Sequence 10382, A
40 202.5 6.2 946 2 US-09-538-092-1230 Sequence 1230, Ap
41 201 6.2 816 2 US-10-104-047-2050 Sequence 2050, Ap
42 200.5 6.2 1702 2 US-09-854-133-434 Sequence 434, App
43 198.5 6.1 645 2 US-10-164-595-40 Sequence 40, Appl
44 197.5 6.1 638 2 US-10-164-595-73 Sequence 73, Appl
45 196 6.0 1041 2 US-09-949-016-9618 Sequence 9618, Ap

QY 301 VPCGKRIKFKGLSKRCDCRVVSHPECDRCPLPCIPITLIGTPVKIGBMLADFVSQTS 360
Db |||||
QY 301 VPCGKRIKFKGLSKRCDCRVVSHPECDRCPLPCIPITLIGTPVKIGBMLADFVSQTS 360
Db |||||
QY 361 MIPSIIVHVCNIEQRLGTETGLYRISGCDRTVVKELKFKLVKTVPLLSKVVDDIHAICS 420
Db |||||
QY 361 MIPSIIVHVCNIEQRLGTETGLYRISGCDRTVVKELKFKLVKTVPLLSKVVDDIHAICS 420
Db |||||
QY 421 LKQDFLNLKPELLTFLRNAPFWEAAETDENSIAAMYQAVGELPOANRDTLAFIMHL 480
Db |||||
QY 421 LKQDFLNLKPELLTFLRNAPFWEAAETDENSIAAMYQAVGELPOANRDTLAFIMHL 480
Db |||||
QY 481 QVAPSPHTKMDVANLAKVFGPTIVAHAVPNPDVMTSODIKRQPKVVERLLSLPLEYWS 540
Db |||||
QY 481 QVAPSPHTKMDVANLAKVFGPTIVAHAVPNPDVMTSODIKRQPKVVERLLSLPLEYWS 540
Db |||||
QY 541 QFMVVEQENIDPLHVIENSNAFSTQTPDIKVSLLGPVTTPEHQLLKTTPSSSSLSQVR 600
Db |||||
QY 541 QFMVVEQENIDPLHVIENSNAFSTQTPDIKVSLLGPVTTPEHQLLKTTPSSSSLSQVR 600
Db |||||
QY 601 TLTKNTPRFGSKSATNLGRQGNFASPMK 632
Db |||||
QY 601 TLTKNTPRFGSKSATNLGRQGNFASPMK 632
Db |||||

RESULT 2

US-09-949-016-7193
; Sequence 7193, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7193
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7193

Query Match 34.9%; Score 1133; DB 2; Length 245;
Best Local Similarity 99.6%; Pred. No. 6.7e-99;
Matches 222; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 349 GMLADFVSQTSMPISIVVHCNIEQRLGTETGLYRISGCDRTVVKELKFKLVKTVPL 408
Db 23 GMLADFVSQTSMPISIVVHCNIEQRLGTETGLYRISGCDRTVVKELKFKLVKTVPL 82
QY 409 LSKVDDIHAICLLKDFLNLKPELLTFLRNAPFWEAAETDENSIAAMYQAVGELPOA 468
Db 83 LSKVDDIHAICLLKDFLNLKPELLTFLRNAPFWEAAETDENSIAAMYQAVGELPOA 142
QY 469 NRDTLAFIMHLQVAPSPHTKMDVANLAKVFGPTIVAHAVPNPDVMTSODIKRQPKV 528
Db 143 NRDTLAFIMHLQVAPSPHTKMDVANLAKVFGPTIVAHAVPNPDVMTSODIKRQPKV 202
QY 529 ERLLSLPLEYWSQFMVVEQENIDPLHVIENSNAFSTQTPDIK 571
Db 203 ERLLSLPLEYWSQFMVVEQENIDPLHVIENSNAFSTQTPDIK 245

RESULT 3

US-09-080-855-2

; Sequence 2, Application US/09080855A
; Patent No. 6083721
; GENERAL INFORMATION:
; APPLICANT: Saras, Jan
; APPLICANT: Franz, Petra
; APPLICANT: Aspenstrm, Pontus
; APPLICANT: Hellman, Ulf
; APPLICANT: Genez, Leonel Jorge
; APPLICANT: Helldin, Carl-Henrik
; TITLE OF INVENTION: PARG, A GTPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PTPL1
; FILE REFERENCE: L0461/7030
; CURRENT APPLICATION NUMBER: US/09/080,855A
; CURRENT FILING DATE: 1998-05-18
; EARLIER APPLICATION NUMBER: 08/805,583
; EARLIER FILING DATE: 1997-02-25
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1261
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-080-855-2

Query Match 9.3%; Score 301; DB 2; Length 1261;
Best Local Similarity 22.4%; Pred. No. 9.4e-19;
Matches 153; Conservative 120; Mismatches 249; Indels 160; Gaps 33;
QY 9 RNLFEQLVRRVVEILSEGNEVQIOLAKDFEDFRKQWQRTDHE-LGKYKDLMLKAEATERSA 67
Db 372 RRLSEELAKQVE---EADLYKV-CVTNVEBRRNDVENTKREILAQLRTLVPQCDLTLKA 427
QY 68 LDVVKLKHARNOVDVEIKRQBAEADCEKLERQIOLIRMLMCDTSGSIQLSSEQK---SA 124
Db 428 VTVNLFTMQLHQAASLADRLQSLCGSAKLYDPGOEYSEFVKATNS-----TEEEKVDGNV 482
QY 125 LAFINRGOPSSNAGNKRLLSTI---DESGSTLSIDISDPKTDSDLDWSSSLVKTFLKKRE 181
Db 483 NKHLNSQPSGFGPANSLDVEDVRLPDSNKIEBRCNSADIT---GPSFRSTWTFMGFS 539
QY 182 KRRSTSRQFVDGPPGVKTRSIGSAVDQGNESIAVAKTTVTVPNDGGPIEAVSTIETVPY 241
Db 540 DSEST-----GSSSESRSLDS-----ESI-----SPGD----- 562
QY 242 WTRSRRTGTLPWNSSDSTLNSRQLEPRTEF--DSVGTPOS---NGMRLHDFVSKTVIK 296
Db 563 FHRKLPRTSSSGTWSADDLDEREPPSPSETGPNLSGTFFKTLMSKAALTHKF--RKLRS 620
QY 297 PESCVPGCKRIKFKGLSKRCDCRVVSHPECDRCPLPC---IP---TLIGTPVKIGEG 349
Db 621 PTKRDCGEGIVVF--QGVCEECLELVCHRKCLENLVVICGHQKLPKHLFG----- 670
QY 350 MLADF--VSQTSMPISIVVHCNIEQRLGTETGLYRISGCDRTVVKELKFKLVKTV 406
Db 671 --AEFTLVAKPEPGIPILKICASEIENRALCLQGIYRVCG-----NKKITE 716
QY 407 PLLSKVD-----DI-----HAICSLKDFLNLKPELLTFLRNAPFWEAAE---ITDE 451
Db 717 KCLALENGHLVDISEFSSHDI CDVLKLYRQLPEPFIPLFRLYKEFIDLAKETQHVNEE 776
QY 452 DNS-----IAAMYQAVGELPOANRDTLAFIMHLQVAP--QSPHTK 490
Db 777 QETKNKSLDKWPNMCIENRILKSKDLRQLRQAPSNFNSLHFLIHLKRVVDHAENK 836
QY 491 MDVANLAKVFGPTIVAHAVPNPD--PVTMSQ--DIKQPKVVERLLSLPLEYWSQFM--- 543
Db 837 MNSXNLGVIFGPSLIR---PRPQTAPITISSLAEYSQARLVEFLIT-----YSQKIFDG 888
QY 544 -MVEQENIDPLHVIENS---NAFSTPQTPDIKVSLLGPVTTPEHQLLKTTPSSSSLSQVR 599
Db 889 SLOPQDVMCSIGVVDQGCFFPKPLSPEDRTIERSMKSLFFSSKEDIHTSESESKIFERAT 948
QY 600 STLTKNTPRFGSKSATNLGR 621

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Db      949 S-----FEESERKQNALGK 962

RESULT 4
US-09-566-076-2
; Sequence 2, Application US/09566076
; Patent No. 6475775
; GENERAL INFORMATION:
; APPLICANT: Sarasz, Jan
; APPLICANT: Franzen, Petra
; APPLICANT: Aspenstrm, Pontus
; APPLICANT: Hellman, Ulf
; APPLICANT: Genez, Leonel Jorge
; APPLICANT: Heldin, Carl-Henrik
; TITLE OF INVENTION: PARG, A GTPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PTPL1
; FILE REFERENCE: L0461/7030
; CURRENT APPLICATION NUMBER: US/09/566,076
; CURRENT FILING DATE:
; EARLIER APPLICATION NUMBER: 09/080,855
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1261
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-566-076-2

Query Match      9.3%; Score 301; DB 2; Length 1261;
Best Local Similarity 22.4%; Pred. No. 9.4e-19;
Matches 153; Conservative 120; Mismatches 249; Indels 160; Gaps 33;

QY      9 RNLPEQLVRRVEILSENEVOFTQLAKDPEDPRKKWQRTDHE-LGKVKDILLMKAETERSA 67
Db      372 RRLLEALQKE---EADELYKV-CVTNVEERNVDVENTKREILAQLRTLVFOCDLTLKA 427

QY      68 LDYKLKHARNQVDVEIKRRQRAEADCEKLERIQILIREMLMCDTSGSIQSEBQK---SA 124
Db      428 VTVNLFMHQLQASLADRLQSLCGSAKLYDPQGEYSEFVKATNS-----TEBEKVDGNV 482

QY      125 LAFNLNQGSSNAGNKRSLSTI---DESGSILSDISFDKTDSDLDNDWSLIVTKFKLKKRE 181
Db      483 NKHLNQQSPGFGFANSLVDVRLPDSNKNKIBEDRCSNSADIT---GPSFIRSWTFGMFS 539

QY      182 KRSTSRQFVGPPGVKTRSGSAVDQGNESIVAKTTVTVPNDGGPIEAUSTIETVPY 241
Db      540 DSEST-----GGSSRSRLDS-----ESI-----SPGD----- 562

QY      242 WTRSRRTGTLPWNSSDTLNSRLQLEPRTE---DSVGTPOS---NGGMRHLDFVSKTVIK 296
Db      563 FHRKLPRTSPSSGTMSSADDLDERPPSPSETGPNLSLGTFFKTLMSKAALTHKP--RKLRS 620

QY      297 PESCPVCGKRIKFGKLSLKCRCDCRVVSHPECRDRCLPC---IP---TLIGTPVKIGEG 349
Db      621 PTKCRDCEGIWFP--QGVCECECLLVCHRRKLENLVICGHQKLPKGKHLFG----- 670

QY      350 MLADF--VSQTSF-MIPSIIVVHCNTEIQRGLTETGLYRISGCDRTVVKELKEFLAVKTV 406
Db      671 --AEFTLVAKBPDGPIFILIKICASEIENRACLCQGIYVCG-----NKKITE 716

QY      407 PLLSKVD-----DI-----HAICSLIKDFLRLNKEPLLTFRLNRAFMEAAE---ITDE 451
Db      717 KLCIALENGHMLVDISEFFSHDIDCVLKLVLRLQPEPFIILFRLYKFIIDLAKELQHVNEE 776

QY      452 DNS-----IAAMYQAVGELPQANRDTLAFMIHLQVRA-QSPHTK 490
Db      777 QETKNSLEDKWPNMCIETNIRLLSKSLQRLQLPASNFSNHLFLIVHLKRVVDHAEENK 836

QY      491 MDVANLAKVGPPTIVAHAVNPD--PVTMSQ---DIRKQPKVVERLLSLPLEYHSQPM--- 543
Db      837 MNSKILGVIFGSLIR---PRPQTAPITISLAEYSNQARLVFLFT-----YSOKIFDG 888

QY      544 -MVEQENIDPLHVIENS--NAFSTPQTPDIKVSLLGPTVTPPEHQLLKTSPSSSLSORVR 599

Db      889 SLQPDVVMCSIGVWDGCGFPKPLLSPEERDIERSMKSLFFSSKEDIHTSESESKIPERAT 948
QY      600 STLTKNTPRFGSKSKSATNLGR 621
Db      949 S-----FEESERKQNALGK 962

RESULT 5
US-09-949-016-9916
; Sequence 9916, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9916
; LENGTH: 838
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9916

Query Match      8.7%; Score 282; DB 2; Length 838;
Best Local Similarity 25.5%; Pred. No. 3e-17;
Matches 140; Conservative 67; Mismatches 201; Indels 140; Gaps 21;

QY      48 DHELQKYLKLLMKAETERSALDVKLKHARNQVDVEIKRRQRAEADCEKLERIQILIREML 107
Db      353 DHEL---EDMKKISALKSEI-----QXKANKGQSR--IERLKKM-PENEFL 396

QY      108 MCDTSGSIQSEBQSKALAFI---NRGPPSSNAGNKRSLSTIDESGSLSDISFKTDE 163
Db      397 LLINGPTIPFRIHNRNGKSYLFLLSSDYERSEWREAIQKQKDLQAFVLSSVELQVLG 456

QY      164 SLDWSSLVTKFKLKKREKRSTSRQFVDPGPPVKKTRSIGSAVDQGNESIVAKTTTV 223
Db      457 S-----CPKLRVTVMHNPVTSNKKDDDESPLGYGLFHLVIVHSAKGFQSANLYCTLEV 507

QY      224 PNDGGPIEAUSTIETVPYWTRSRRTK---GTLQP-WNS----- 257
Db      508 DSFG-----YFV-SKAKTRVPRDTAEPKMDSEFEIELBGSQSLRLCYEKCY 553

QY      258 DSTLNSR-----QLBPRT-ETDSVGTPOSGMRHLHDFVSKTVIKESCV 301
Db      554 DTKTKVNKNNEIVDKIMGKQIQLDPPQTVETKNWHT-----DVIEMNGIKVEFSM 603

QY      302 PCGKRIFKGLSKICEDCHRVSHPECRDRCLPCIPITLIGTPVKIGEGMLADFVS---Q 357
Db      604 KFTSR---DMSLK-----RTPSKKQTGVGVKISVVTKR 634

QY      358 TSPMIPSIIVVHCNTEIQRGLTETGLYRISGCDRTVVKELKEF-LRVKTVPLLSKVDIH 416
Db      635 ERSKVPYIVRQCVEEVEKGIIEVGIYRISGVATDIQALKAVFDANNKILLMLSDMDIN 694

QY      417 AICSLIKDFLRLNKEPLLTFRLNRAFMEAAEITDEDNSIAAMYQAVGELPQANRDTLAF 476
Db      695 AIAGTLKLYFRELPEPLTDRLYPAPMEGIALSDPAAKENCMHLLRSLPDPNLITFLEL 754

QY      477 MIHLQVRAQ-SPTKMDVANLAKVGPPTIV-----AHAVNPDPVMTSQDIKQPKV 527
Db      755 LEHLKRVAEKPEINKMSLNLTATVGPITLLRPFSEVESKAHLTSAAD--TWSHDVMVAQVQV 812
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QY 528 VERLLSLP 535
Db 813 LLYYLQHP 820

RESULT 6

US-09-949-016-9917
; Sequence 9917, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9917
; LENGTH: 838
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9917

Query Match 8.7%; Score 282; DB 2; Length 838;
Best Local Similarity 25.5%; Pred. No. 3e-17; Mismatches 201; Indels 140; Gaps 21;
Matches 140; Conservative 67; Mismatches 201; Indels 140; Gaps 21;

QY 48 DHELKGYKDLLMKAETERSALDVKLKHARNQVDVEIKRQRAEADCEKLEROIQLIREML 107
Db 353 DHEL---EDMKKISALKSEI-----QEKANKGOSRA---IERLKQKQ-PENEF 396
QY 108 MCDTSGSIQSEQKSAFL-----NRGQSSNAGNKRSLTIDSGSILSDISPKTDE 163
Db 397 LLNLSPTIPFRHNRNGSKSYLLSSDYERSEWREAIQKQKDLQAFVLSSVELQVLGT 456
QY 164 SLDDSSLVKTKLKKREKRSTSQFVDPGPGPVKKTSGSAVDQGNESIVAKTTTV 223
Db 457 S-----CPKLRTHVNIPIVTSNKKDDDESPLGYGLFHLVIVHSAKGFQSANLYCTLEV 507
QY 224 PNDGGPIEAVSTIETVPYTRRRKT---GTLQP-WNS----- 257
Db 508 DSFG-----YFV-SKATRVPRDTAEPKWDEEFIELEGSQSLRLCYEKY 553
QY 258 DSTLNSR-----QLRPRT-ETDSVGTPOSNGMRLHDFVSKTVIKPESCV 301
Db 554 DKTQVKNKDNNEIVDKIMGKQIQLOPQTVETKNWHT-----DVIEMNGIKVFP 603
QY 302 PGCKRIKFKGLSKCEDCHVSHPECDRCPLCPIPTLIGTPVKIGEGMLADFVS---Q 357
Db 604 KFTSR-----DMSLK-----RTPSKKQTVGVGVKISVVTKR 634
QY 358 TSPMIPSIYVHCNTEIQRGLTETGLYRISGCDRTVVKELKEKF-LRVKTVPLLSKVDDIH 416
Db 635 ERSKVPYIVROCVEVEKKGIEVGIYRISGVATDIQALKAFVFNKDVNNKDVMMSEMDVN 694
QY 417 AICSLKDLFLRNKLEPLLTFRLNRAFMEAAEITDEDSNIAAMYQAVGELPOANRDTLAF 476
Db 695 AIAGTLKLYFRELPEPLTDRLYPAFMEGIALSDPAKENCMHLLRSLPDNLTITFL 754
QY 477 MHLQORVAQ-SPTKMDVANLAKVGPPIV-----AHAVNPDPVTMSODIKRQKV 527
Db 755 LEHLKRVAEKEPINKKSLNLTATVFGPTLLRPSVESKAHLTSAAD--IWSHDVMAQVQV 812
QY 528 VERLLSLP 535
Db 813 LLYYLQHP 820

RESULT 7

US-09-949-016-11527
; Sequence 11527, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11527
; LENGTH: 1287
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11527

Query Match 8.7%; Score 281.5; DB 2; Length 1287;
Best Local Similarity 22.8%; Pred. No. 6.9e-17; Mismatches 139; Conservative 93; Mismatches 211; Indels 167; Gaps 28;

QY 19 VEILSEGNVQFIQAKDF-----EDFRKKW-----QRTDHELKGYK 55
Db 732 VELVEGARKLRHVFLLFTDLLCTKLKQSGKQYQYCKWYIPLTDLFSQMYD-ELEAVP 790
QY 56 DLLMKAETERSALDVKLKHARNQVDVEIKRQRAEADCEKLEROIQLIREMLCMTSGSI 115
Db 791 NIPVPEELDALIKISQIKNDIQRE-KRANKGSKATERLKKKL----- 834
QY 116 QLSBEQKSAFLNRGQSSNAGNKRSLTIDSGSILSDISFKTDSLSLWDSLSLVKTF 175
Db 835 ---SEQESLLLSLSPSMAFRVHRSNGKSYTF---LISSDY-----ERAEWRENI--- 877
QY 176 KLKREKRSTSRQFVDPGPGPVKKTSGSAVDQ--GNESIVAKTTTVTP-----NDG 227
Db 878 ---REQQKKCFRSGF-----SLTSVELQMLTNSCVKLTQVHSIPTLTINKEDDE 921
QY 228 GP-----IEAVSTIETVPYW---TRSRRTGTLPQ-WNSDSTL- 261
Db 922 SPGLYGLFNLVIVHSATGFKQSSNLYCTLEVDSFGYFVNKAKTRVYRDTAEFNWNEEPEIE 981
QY 262 ---NSRQLE-----PRTETDSVGTPOSNGMRL-----HDFVSKTVIKPES 299
Db 982 LEGSQTLLRILCYEKNKTIKIPKEDGESTDLRMKGQVQLDPQALQDRDW-QRTVIAMNG 1040
QY 300 CVPCKRIKFG--KLSLKRCDCRVVSHPECDRCPLCPIPTLIGTPVKIGEGMLADFVSQ 357
Db 1041 -IEVLSYKFNRSRREFSLK-----RMPESRQKTGVFG--VKI-----AVVTKR 1078
QY 358 TSPMIPSIYVHCNTEIQRGLTETGLYRISGCDRTVVKELKEKF-LRVKTVPLLSKVDDIH 416
Db 1079 ERSKVPYIVROCVEIEERRGMEVGIYRISGVATDIQALKAFVFNKDVNNKDVMMSEMDVN 1138
QY 417 AICSLKDLFLRNKLEPLLTFRLNRAFMEAAEITDEDSNIAAMYQAVGELPOANRDTLAF 476
Db 1139 AIAGTLKLYFRELPEPLTDFYFNFAEGIALSDPVAKESQWLNLLSLPEANLLTFLFL 1198
QY 477 MHLQORVAQSPH-TKMDVANLAKVGPPIV-----AHAVNPDPVTM---SODIKRQ 524
Db 1199 LDHLKRVAEKBAVNMKSLNLTATVFGPTLLRPSKEKSLPANPSQPIITMTDSWSLEVMSQ 1258
QY 525 PKVVERLLSL 534
Db 813 LLYYLQHP 820

Db 1259 VQVLLYFLQL 1268

RESULT 8

US-09-949-016-7008

; Sequence 7008, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CLO01307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 7008

; LENGTH: 1227

; TYPE: PRT

; ORGANISM: Human

US-09-949-016-7008

Query Match 8.6%; Score 278.5; DB 2; Length 1227;

Best Local Similarity 23.5%; Pred. No. 1.2e-16;

Matches 138; Conservative 89; Mismatches 195; Indels 165; Gaps 28;

Qy 19 VEILSEGNEVQFIQAKDF-----EDPRKKW-----ORTDHELKGYK 55

Db 716 VELVEGARKUNHFLFTDLLLCTKQKSGKTOYQCKWYPIPLDLSFQWVD-ELEAVP 774

Qy 56 DLLMKAETERSALDVKLHARNQVDVEIKRRQAEADCEKLERQIQIIREMLMCDTSGSI 115

Db 775 NIPLVPBDELDAIKI-----SQIKSDIQREKANKGSKATER-----LKKKL----- 818

Qy 116 QLSEQKSAFLNRPQSSNAGNKLSTIDSGSILSDISFKTDDESIDWSSLVKTF 175

Db 819 ---SEQESLLMLGSPMAFRVHSRNGSKSYTF-----LISSDY-----ERAEMRENI----- 861

Qy 176 KLKREKRSTSRQFVDPGPPGVKTRSIGSAVDQ---GNESIVAKTIVTVVP-----NDG 227

Db 862 -----REQOKCFRSF-----SLTSVELQMLTNSCVKLOTVHSLPLINKEDDE 905

Qy 228 GP-----IEAVSTIETVPYW---TRSRKTKTLOP-WNSDSLTLN 262

Db 906 SPGLYGLFNLVIVHSATGFKQSSNLYCTLEVDSPGYFNKAKTRVYRDTAEPNWN----- 959

Qy 263 SRQLEPRTETSDVGTPOSGMRLHDFVSKTVIKPESCVPGKRIKFG---KLSLKCRDCR 320

Db 960 ---ELDPQALQD-----RDW-QRTVIAMNG-IEVKLSVKFNSREFSLK----- 997

Qy 321 VVSHPECDRCPLCPIPLTIGTPKIGEGMLADFVSQTSPIPSIVHVCNIEIQRGILTE 380

Db 998 -----RMPRSKQTVGFG--VKI-----AVVTKRSKVPVIVRQCVEEIERRGWEE 1041

Qy 381 TGLYRISGCDRTVKELKEF--LRVKTVPLLSKVDIIHAIICSLLDKFLRNKEPILLTERLN 439

Db 1042 VGIYRVSGVATDIALKAFAFVNKNKDVSMSEMDVNAIAGTLKLYFRELPEPLFTDEFY 1101

Qy 440 RAFMEAAEITDSDNSIAAMYQAVGELPOANRDTLAFMLHILQVQAQSPH-TKMDVANLAK 498

Db 1102 PNFAEGIALSDPAKESCMILLLSLPEANLLTFLFLDLHLKRVAEKEAVNKNLSHLNAT 1161

Qy 499 VFGPTIV-----AHAVPNP-DPVTM-----SQDIKRPQKVVERLISL 534

Db 1162 VFGPTLLRPSKESKLPANPSQPTITMTDSNLSLEVMQVQLLYFLQL 1208

RESULT 9

US-09-172-422-1

; Sequence 1, Application US/09172422A

; Patent No. 6300485

; GENERAL INFORMATION:

; APPLICANT: Adams, Arwen E.

; APPLICANT: Chiu, Choi Ying

; APPLICANT: Duhl, David

; APPLICANT: Gorman, Susan W.

; APPLICANT: Leng, Song

; APPLICANT: Sheffield, Val

; APPLICANT: Welch, Juliet

; TITLE OF INVENTION: MYOSIN IXA AND CYCLIC NUCLEOTIDE GATED

; TITLE OF INVENTION: CHANNEL-15 (CNGC-15) POLYNUCLEOTIDES, POLYPEPTIDES,

; TITLE OF INVENTION: COMPOSITIONS, METHODS, AND USES THEREOF

; FILE REFERENCE: 200130.442

; CURRENT APPLICATION NUMBER: US/09/172,422A

; CURRENT FILING DATE: 1998-10-14

; NUMBER OF SEQ ID NOS: 3

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1

; LENGTH: 2548

; TYPE: PRT

; ORGANISM: Homo sapien

US-09-172-422-1

Query Match 8.3%; Score 270.5; DB 2; Length 2548;

Best Local Similarity 24.4%; Pred. No. 2.4e-15;

Matches 130; Conservative 75; Mismatches 203; Indels 125; Gaps 24;

Qy 143 LSTIDSGSILSDISFKTDDESIDWSSLVKTFKLKREKRSTSRQFVDGPPGVKTR 202

Db 1864 LKSMDS--ELLKKVN-DLDNEDSKKDTLVVDVVFKKALKEFRQN-----IFSFY 1908

Qy 203 SIGSAVDQGN-----ESIVAKTIVTVVPNDG---GPIEA-VSTIETVPVWTRSR 247

Db 1909 SSALAMDDGKSTIRKDYALFEQILEKTMRLQORDSLGSPVRVWNTTKVFLDEYWNEF 1968

Qy 248 KTGTLPWNSSDTL-----NSRQLEPRTETSDVGTPOSGMRLHDFVSKTVIKPESCV 302

Db 1969 KT-----SDCTATKVPKTERKKRKKETDLV--BEHNG-----HIFKATQYSIPTCY 2015

Qy 303 CGKRIKFGKLSLKCRDCRVVSHPECDRCPLCPIPLTIGTPVKIGE-----GMLADFV 355

Db 2016 CSSLIWIMDRASVCKLCKYACHKC-----CLKTTAKCSKKYDPELSSRQFGVLSRL 2068

Qy 356 SQTSPIPSIVHVCNIEIQRGILTEGLYRISGCDRTVKELKEFLRVKTVPLLSKVD-- 414

Db 2069 TSEDRTVPLVVEKLIINYIEMHGLYTEGIVRKSGSTNKKIKELQ---GLDIDAESVNLDDY 2125

Qy 415 -HAIICSLKDFURNLKEPLLTPFLNRAFWAAEITDSDNSIAAMYQAVGELPOANRDTL 473

Db 2126 NIHVIAVFKQWLRLDLPNPLMTFELYEEFLRANGLOERKETIRGVYSVIDQLSRHLNTL 2185

Qy 474 AFLMIHLQVA-QSPHTKMDVANLAKVFGPTIVVAHAVPNPDPVMTSQDIKRPQKVVERLL 532

Db 2186 ERLIFHLVRIALQEDTNRMSANALAVFAPCIL-RCPDITDPLQSQVDISKTTTCVE--- 2241

Qy 533 SLPLETWSQFMVVEQN-----IDPLHVIENSNAFSTPQTPFDIKVSL-- 575

Db 2242 -----LIVVEQNNKYKARKLDISSLFEAENK-----AKTRLSLIRSMGKGR 2284

Qy 576 -----GPVTTPEHQLLKTTPSSSSLSQRVSRSTLTNKTPTFRGSKSKSATNLGRQ 622

Db 2285 RRGNYFGP-SSP--VVVRLPSVSDVSE---EYLT-----SEAMETDITEQ 2324

RESULT 10

US-09-949-016-6235

; Sequence 6235, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

Query Match 7.8%; Score 254.5; DB 2; Length 748;
Best Local Similarity 26.0%; Pred. No. 1e-14;
Matches 113; Conservative 61; Mismatches 183; Indels 77

Db 135 EVQE---SKNFNIVEPVLAFLHLSFISNSLTVELTDFLPYKQQL--QLSLQNRNHFSS 189
Qy 187 SRQVDPGPGPVKTRSIGSAVDOGNESIVAKTIVTPNDGGP-IEA-----VSTIE 237
Db 190 TREEMELKKRMKE-----APQCKLP--GQPTIEGYLTQKQWALGIS 231
Qy 238 TVPVWTSRRKTGTLQPNWSDSTLNSRQLSPRTETDSVGPQSGMRLHDFVSKTVIKP 297
Db 232 WVKYCYQYKTKL-----TWPMEQRP-----GAKQPLDLTLKYCVR---KT 274
Qy 298 ESCVPCGKRIKFGKLSLKRCDCRVVSHP-----ECRDRCP LPCI---PTLIGTPVK 345
Db 275 ES-----IDKRP-----CFDIETNERPGTITLQALSEANRRLWMEAMDGKEPIYHSPIT 323
Qy 346 IGEQMLADFVSQSPMTIPSVVHCNVEIORGLTETGLYRISGCDRTVKELKEKFLRVK- 404
Db 324 KQEMELNEVG-----KFRVKCINIETKGIKTEGLYRTVGSNIQVQKLLNAFFDPKC 377
Qy 405 --TVPLLSKVDDIHAICSLKDFLRLNKEPLTLFRLNRAFMEAAEITDEDNSIAAMYQAV 462
Db 378 PGDVDFHNSWDIKTITSSLSKFLYRLNLEPMTYRLHKELVSAKSDNLDYRLGAHSLV 437
Qy 463 GELPQANRDLAFIMHILQOVAOSPTK---MDVANLAKVFGPTIVAHAVNPDPVPTMSQ 519
Db 438 YKLEKREMELELIRHLNVCE--HSENLMTPSNMGVIFGPTLMR---AQEDTVAAMM 492
Qy 520 DIKQPKVVERLLSLPLEYWSQFM--VEQENIDPL-----HVIENS 560
Db 493 NIKFQNIWVEIL-----IEHFGKIYLGPPESAAPPVPPRVATARRHKPITISKRLLRERT 548
Qy 561 AFSTP-----QTPDIKV-SLGLPVTTPHQLL-----KTPSS----- 591
Db 549 VFYTSLSDESEDEIQHTPNGTITSSIEPPKPPQHPKLPQIRSGETDPGRKSPRPILDG 608
Qy 592 -----SSLSQVRSTLTNTNTPFGSKSATN 618
Db 609 KLEPCPEVDYVKLVRLQDGGTKITPK-----ATN 638

RESULT 15

US-10-080-960-32
; Sequence 32, Application US/10080960
; Patent No. 6979564
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Glucksmann, Maria
; APPLICANT: Meyers, Rachel
; TITLE OF INVENTION: 80090, 52874, 52880, 63497, AND 33425
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF HUMAN
; TITLE OF INVENTION: PROTEINS AND USES THEREOF
; FILE REFERENCE: 38155-20044.00
; CURRENT APPLICATION NUMBER: US/10/080,960
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/242,040
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/242,038
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/241,992
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/242,637
; PRIOR FILING DATE: 2000-10-23
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus amino acid
US-10-080-960-32

Query Match 7.7%; Score 251; DB 2; Length 170;
Best Local Similarity 39.8%; Pred. No. 1.8e-15;

Matches 64; Conservative 27; Mismatches 52; Indels 18; Gaps 5;
Qy 363 PSIVVHCVNEIE-----QRLTETGLYRISGCDRTVKELKEKFLRVKTVPLLSKVD--- 413
Db 1 PIIVEKCVYIEIKLYPLAERGLQEEGIYRVSGASRVKELREAFDKDGAPDSLELSEKEW 60
Qy 414 -DIHAICSLKDFLRLNKEPLTLFRLNRAFMEAA--EITDEDNSIAAMYQAV-GELPQAN 469
Db 61 FDVHVVAGLLKLYLRELPEPLIPYDLIEFIRAAKEQIEDPDERLALAKELLSSKLPRAH 120
Qy 470 RDTLAFIMHILQOVAQ-----SPHTKMDVANLAKVFGPTIV 505
Db 121 YNTLRVLLTHLNRAVEIYIENSANVKNMARNLAIVFGPTLL 161

Search completed: August 9, 2006, 16:23:32
Job time : 53 secs

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OM protein - protein search, using sw model

Run on: August 9, 2006, 16:34:05 ; Search time 185 Seconds
(without alignments)
1582.442 Million cell updates/sec

Title: US-09-881-736A-2
Perfect score: 3243
Sequence: 1 MDTMMLNVRNLFQLVRRVE.....SKSATNLGROGNFFASPMKX 632

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3243	100.0	632	3	US-09-881-736-2
2	3237	99.8	632	5	US-10-287-436A-408
3	3237	99.8	632	5	US-10-287-436A-1106
4	3230	99.6	632	3	US-09-833-790-413
5	3230	99.6	632	5	US-10-756-149-5722
6	2919	90.0	570	3	US-09-833-790-427
7	2734	84.3	628	3	US-09-881-736-4
8	1182	36.4	255	4	US-10-408-765A-1045
9	864	26.6	625	6	US-11-097-143-30960
10	625	19.3	4318	5	US-10-450-763-45146
11	618	19.1	665	5	US-10-450-763-40589
12	618	19.1	1086	5	US-10-450-763-50263
13	618	19.1	1139	5	US-10-450-763-44317
14	541.5	16.7	384	6	US-09-881-736-6
15	477	14.7	384	6	US-11-097-143-4533
16	334	10.3	2022	4	US-10-408-765A-598
17	322	9.9	175	4	US-10-072-012-878
18	322	9.9	175	4	US-10-072-012-879
19	310	9.6	1261	4	US-10-072-012-733
20	301	9.3	1261	4	US-10-177-980-2
21	301	9.3	1261	6	US-10-648-593-192
22	301	9.3	1261	6	US-11-072-175-192
23	294.5	9.1	193	3	US-09-802-127-8
24	294	9.1	295	4	US-10-205-194-95
25	294	9.1	1019	5	US-10-487-092-11
26	290.5	9.0	759	5	US-10-450-763-47152
27	290.5	9.0	800	5	US-10-450-763-47153

28	290.5	9.0	814	5	US-10-781-581-185	Sequence 185, App
29	290.5	9.0	814	5	US-10-756-149-5188	Sequence 5188, Ap
30	290.5	9.0	926	5	US-10-499-065A-531	Sequence 531, App
31	286.5	8.8	718	4	US-10-087-192-333	Sequence 333, App
32	286.5	8.8	1173	4	US-10-072-012-725	Sequence 725, App
33	286.5	8.8	1286	4	US-10-153-668-212	Sequence 212, App
34	286.5	8.8	1286	4	US-10-072-012-724	Sequence 724, App
35	286.5	8.8	1354	4	US-10-153-668-470	Sequence 470, App
36	286.5	8.8	1958	5	US-10-483-506-19	Sequence 19, Appl
37	285.5	8.8	996	4	US-10-072-012-731	Sequence 731, App
38	285.5	8.8	1136	4	US-10-072-012-729	Sequence 729, App
39	285.5	8.8	1165	4	US-10-072-012-730	Sequence 730, App
40	285.5	8.8	1192	4	US-10-369-493-3502	Sequence 3502, Ap
41	284.5	8.8	1136	4	US-10-072-012-280	Sequence 280, App
42	284	8.7	1355	4	US-10-072-012-278	Sequence 278, App
43	283.5	8.7	1270	5	US-10-840-512-127	Sequence 127, App
44	278.5	8.6	967	5	US-10-450-763-42547	Sequence 42547, A
45	278.5	8.6	1227	5	US-10-918-648-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-09-881-736-2
; Sequence 2, Application US/09881736
; Patent No. US20020076785A1
; GENERAL INFORMATION:
; APPLICANT: Glotzer, Michael
; APPLICANT: Jantech-Plunger, Verena
; APPLICANT: Romano, Alper
; APPLICANT: Mishima, Masanori
; APPLICANT: Kaitna, Susanne
; TITLE OF INVENTION: Cyk-4 polypeptides, DNA molecules encoding them and their use in
; TITLE OF INVENTION: screening methods
; FILE REFERENCE: 0652.2260001/EKS/AES
; CURRENT APPLICATION NUMBER: US/09/881,736
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: EP 00 112 880.0
; PRIOR FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: EP 01 110 554.1
; PRIOR FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 60/241,231
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: To be determined
; PRIOR FILING DATE: 2001-06-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; TYPE: PRT
; LENGTH: 632
; ORGANISM: Homo sapiens
US-09-881-736-2

Query Match 100.0%; Score 3243; DB 3; Length 632;
Best Local Similarity 100.0%; Pred. No. 3.1e-258;
Matches 632; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MDTMMNLNVRNLFQLVRRVEILSEGNVQPIQAKDFEDFRKKWQRTDHELGYKDLLMK	60
Db	1	MDTMMNLNVRNLFQLVRRVEILSEGNVQPIQAKDFEDFRKKWQRTDHELGYKDLLMK	60
Qy	61	AETERSALDVKLKHARNQVDVEIKRQRAEDCEKLERQILIREMLMCDTSGSIQSEE	120
Db	61	AETERSALDVKLKHARNQVDVEIKRQRAEDCEKLERQILIREMLMCDTSGSIQSEE	120
Qy	121	QKSALAFNLNRQSPSSNAGNKRSLSTIDESGSIISDTSFDTKDSLDWSSLVTKFKKR	180
Db	121	QKSALAFNLNRQSPSSNAGNKRSLSTIDESGSIISDTSFDTKDSLDWSSLVTKFKKR	180
Qy	181	EKRSTSRQFVDPGPGPVKKTSTRIGSADGNSIVAKTTVTVPNDGPIEAVSTIETVP	240
Db	181	EKRSTSRQFVDPGPGPVKKTSTRIGSADGNSIVAKTTVTVPNDGPIEAVSTIETVP	240

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QY 241 YWTRSRKGTGLQPNWSDSTLNSRQLEPRTETDSVGTPOSGMRLHDFVSKTVIKPESC 300
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|
|
Db 241 YWTRSRKGTGLQPNWSDSTLNSRQLEPRTETDSVGTPOSGMRLHDFVSKTVIKPESC 300
|
|
|
QY 301 VPCGKRIKFKGLSLKCRDCRVVSHPECDRCPLPCPTLTIGTPVKIGEGMLADFVSQTSP 360
|
|
|
Db 301 VPCGKRIKFKGLSLKCRDCRVVSHPECDRCPLPCPTLTIGTPVKIGEGMLADFVSQTSP 360
|
|
|
QY 361 MIPSIIVHVCNEIEQRLTETGLYRISGCDRTVKELKEKFLRVKTVPLLSKVDDIIHAICS 420
|
|
|
Db 361 MIPSIIVHVCNEIEQRLTETGLYRISGCDRTVKELKEKFLRVKTVPLLSKVDDIIHAICS 420
|
|
|
QY 421 LKXDFLNLKEPLLTFRLNRAFMEAAEITDEDNSIAAMYQAVGELPQANRDTLAFMIHL 480
|
|
|
Db 421 LKXDFLNLKEPLLTFRLNRAFMEAAEITDEDNSIAAMYQAVGELPQANRDTLAFMIHL 480
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|
|
QY 481 QRVASPHTKMDVANLAKVFGPTIVAHAVPNPDVMTSODIKRQPKVVERLLSLPLEYWS 540
|
|
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Db 481 QRVASPHTKMDVANLAKVFGPTIVAHAVPNPDVMTSODIKRQPKVVERLLSLPLEYWS 540
|
|
|
QY 541 QFMVVEQENIDPLHVIENSNAFSTPTQPDIKVSLGPGVTTPEHQLLKTSPSSSLSORVRS 600
|
|
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Db 541 QFMVVEQENIDPLHVIENSNAFSTPTQPDIKVSLGPGVTTPEHQLLKTSPSSSLSORVRS 600
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QY 601 TLTNTPRFGSKSATNLGRQGNFFASPMK 632
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Db 601 TLTNTPRFGSKSATNLGRQGNFFASPMK 632
|
|
|
RESULT 2
US-10-287-436A-408
; Sequence 408, Application US/10287436A
; Publication No. US20050202421A1
; GENERAL INFORMATION:
; APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS
; FILE REFERENCE: 10872.514696
; CURRENT APPLICATION NUMBER: US/10/287,436A
; CURRENT FILING DATE: 2002-10-31
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 1446
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 408
; LENGTH: 632
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-436A-408

Query Match 99.8%; Score 3237; DB 5; Length 632;
Best Local Similarity 99.8%; Pred. No. 9.6e-258;
Matches 631; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDTMMLNVRNLFQQLVRRVEILSEGNEVQFIQLAKDFEDFRKKWQRTDHELKGYKOLLMK 60
|
|
|
Db 1 MDTMMLNVRNLFQQLVRRVEILSEGNEVQFIQLAKDFEDFRKKWQRTDHELKGYKOLLMK 60
|
|
|
QY 61 AETERSALDVKLKHARNQVDVEIKRRQRAEADCEKLERQILIREMLMCDTSGSIQLEES 120
|
|
|
Db 61 AETERSALDVKLKHARNQVDVEIKRRQRAEADCEKLERQILIREMLMCDTSGSIQLEES 120
|
|
|
QY 121 QKSALAFNLGRQSSNAGNKRLLSTIDESGSLSDISFDKTDLSLWDSLVKTFKLKKR 180
|
|
|
Db 121 QKSALAFNLGRQSSNAGNKRLLSTIDESGSLSDISFDKTDLSLWDSLVKTFKLKKR 180
|
|
|
QY 181 EKRSTSRQFVDPGPPGVKTRTSGSAVDQGNESIVAKTTVTPNDGGPIEAVSTIETVP 240
|
|
|
Db 181 EKRSTSRQFVDPGPPGVKTRTSGSAVDQGNESIVAKTTVTPNDGGPIEAVSTIETVP 240
|
|
|
QY 241 YWTRSRKGTGLQPNWSDSTLNSRQLEPRTETDSVGTPOSGMRLHDFVSKTVIKPESC 300
|
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Db 241 YWTRSRKGTGLQPNWSDSTLNSRQLEPRTETDSVGTPOSGMRLHDFVSKTVIKPESC 300
QY 301 VPCGKRIKFKGLSLKCRDCRVVSHPECDRCPLPCPTLTIGTPVKIGEGMLADFVSQTSP 360
|
|
|
Db 301 VPCGKRIKFKGLSLKCRDCRVVSHPECDRCPLPCPTLTIGTPVKIGEGMLADFVSQTSP 360
|
|
|
QY 361 MIPSIIVHVCNEIEQRLTETGLYRISGCDRTVKELKEKFLRVKTVPLLSKVDDIIHAICS 420
|
|
|
Db 361 MIPSIIVHVCNEIEQRLTETGLYRISGCDRTVKELKEKFLRVKTVPLLSKVDDIIHAICS 420
|
|
|
QY 421 LKXDFLNLKEPLLTFRLNRAFMEAAEITDEDNSIAAMYQAVGELPQANRDTLAFMIHL 480
|
|
|
Db 421 LKXDFLNLKEPLLTFRLNRAFMEAAEITDEDNSIAAMYQAVGELPQANRDTLAFMIHL 480
|
|
|
QY 481 QRVASPHTKMDVANLAKVFGPTIVAHAVPNPDVMTSODIKRQPKVVERLLSLPLEYWS 540
|
|
|
Db 481 QRVASPHTKMDVANLAKVFGPTIVAHAVPNPDVMTSODIKRQPKVVERLLSLPLEYWS 540
|
|
|
QY 541 QFMVVEQENIDPLHVIENSNAFSTPTQPDIKVSLGPGVTTPEHQLLKTSPSSSLSORVRS 600
|
|
|
Db 541 QFMVVEQENIDPLHVIENSNAFSTPTQPDIKVSLGPGVTTPEHQLLKTSPSSSLSORVRS 600
|
|
|
QY 601 TLTNTPRFGSKSATNLGRQGNFFASPMK 632
|
|
|
Db 601 TLTNTPRFGSKSATNLGRQGNFFASPMK 632
|
|
|
RESULT 3
US-10-287-436A-1106
; Sequence 1106, Application US/10287436A
; Publication No. US20050202421A1
; GENERAL INFORMATION:
; APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS
; FILE REFERENCE: 10872.514696
; CURRENT APPLICATION NUMBER: US/10/287,436A
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/336,220
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 1446
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1106
; LENGTH: 632
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-436A-1106

Query Match 99.8%; Score 3237; DB 5; Length 632;
Best Local Similarity 99.8%; Pred. No. 9.6e-258;
Matches 631; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDTMMLNVRNLFQQLVRRVEILSEGNEVQFIQLAKDFEDFRKKWQRTDHELKGYKOLLMK 60
|
|
|
Db 1 MDTMMLNVRNLFQQLVRRVEILSEGNEVQFIQLAKDFEDFRKKWQRTDHELKGYKOLLMK 60
|
|
|
QY 61 AETERSALDVKLKHARNQVDVEIKRRQRAEADCEKLERQILIREMLMCDTSGSIQLEES 120
|
|
|
Db 61 AETERSALDVKLKHARNQVDVEIKRRQRAEADCEKLERQILIREMLMCDTSGSIQLEES 120
|
|
|
QY 121 QKSALAFNLGRQSSNAGNKRLLSTIDESGSLSDISFDKTDLSLWDSLVKTFKLKKR 180
|
|
|
Db 121 QKSALAFNLGRQSSNAGNKRLLSTIDESGSLSDISFDKTDLSLWDSLVKTFKLKKR 180
|
|
|
QY 181 EKRSTSRQFVDPGPPGVKTRTSGSAVDQGNESIVAKTTVTPNDGGPIEAVSTIETVP 240
|
|
|
Db 181 EKRSTSRQFVDPGPPGVKTRTSGSAVDQGNESIVAKTTVTPNDGGPIEAVSTIETVP 240
|
|
|
QY 241 YWTRSRKGTGLQPNWSDSTLNSRQLEPRTETDSVGTPOSGMRLHDFVSKTVIKPESC 300
|
|
|
Db 241 YWTRSRKGTGLQPNWSDSTLNSRQLEPRTETDSVGTPOSGMRLHDFVSKTVIKPESC 300
|
|
|
QY 301 VPCGKRIKFKGLSLKCRDCRVVSHPECDRCPLPCPTLTIGTPVKIGEGMLADFVSQTSP 360
|
|
|
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Db 301 VPCGKRIKFGKLSLKCRCRCRVVSHPECDRCPLPCIPTLIGTPVKIGEGMLADFVSQTS 360
Qy 361 MIPSIVVHCVNEIEQRLGTETGLYRISGCDRTVKELKEKFLRVKTVPLLSKVDDIHAICS 420
Db 361 MIPSIVVHCVNEIEQRLGTETGLYRISGCDRTVKELKEKFLRVKTVPLLSKVDDIHAICS 420
Qy 421 LKDFLRLNKEPLLTFRNLRAFMEAAEITDSDNSIAAMYQAVGELPOANRDTLAFMIHL 480
Db 421 LKDFLRLNKEPLLTFRNLRAFMEAAEITDSDNSIAAMYQAVGELPOANRDTLAFMIHL 480
Qy 481 ORVAQSPHTKMDVANLAKVFGPTTVAHAVPNPDVTHMSQDIKROPKVVVERLLSLPLEYWS 540
Db 481 ORVAQSPHTKMDVANLAKVFGPTTVAHAVPNPDVTHMSQDIKROPKVVVERLLSLPLEYWS 540
Qy 541 QFMVVEQENIDPLHVIENSNAFSTPQTDIKVSLGPGVTTPEHQLLKTSPSSSSLSQVRVS 600
Db 541 QFMVVEQENIDPLHVIENSNAFSTPQTDIKVSLGPGVTTPEHQLLKTSPSSSSLSQVRVS 600
Qy 601 TLTKNTPRFGSKSKSATNLGRQGNFFASPMLK 632
Db 601 TLTKNTPRFGSKSKSATNLGRQGNFFASPMLK 632

RESULT 4

US-09-833-790-413
; Sequence 413, Application US/09833790
; Patent No. US20020068288A1
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Wang, Tongtong
; APPLICANT: Secretist, Heather
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Indirias, Carol Y.
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.512
; CURRENT APPLICATION NUMBER: US/09/833,790
; CURRENT FILING DATE: 2001-04-11
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 413
; LENGTH: 632
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-790-413

Query Match 99.6%; Score 3230; DB 3; Length 632;
Best Local Similarity 99.7%; Pred. No. 3.6e-257;
Matches 630; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 MDTMMLNVRNLFEOQLVRRVEILSEGNEVQFIQLAKDPEDFRKKWQRTDHELKGYKDLIMK 60
Db 1 MDTMMLNVRNLFEOQLVRRVEILSEGNEVQFIQLAKDPEDFRKKWQRTDHELKGYKDLIMK 60
Qy 61 AETERSALDVKLKHARNQVDVEIKRQRAEADCEKLEQIQLIREMLMCDTSGSIQJSEE 120
Db 61 AETERSALDVKLKHARNQVDVEIKRQRAEADCEKLEQIQLIREMLMCDTSGSIQJSEE 120
Qy 121 QKSALAFNLNRQSPSSNAGNKRSLTIDSGSILSDISFDKTDDESILWDSLSLVKTFKLKCR 180
Db 121 QKSALAFNLNRQSPSSNAGNKRSLTIDSGSILSDISFDKTDDESILWDSLSLVKTFKLKCR 180
Qy 181 EKRRSTSRQFVDPGPPGVKKTRSIGSAVDQGNESIVAKTTVTPVNDGPGPIEAVSTIETVP 240
Db 181 EKRRSTSRQFVDPGPPGVKKTRSIGSAVDQGNESIVAKTTVTPVNDGPGPIEAVSTIETVP 240
Qy 241 YWTRSRRTGTLOPWNSTLNSRQLEPRTETSDVGTQPSNGMRLHDFVSKTVIKPESC 300
Db 241 YWTRSRRTGTLOPWNSTLNSRQLEPRTETSDVGTQPSNGMRLHDFVSKTVIKPESC 300
Qy 301 VPCGKRIKFGKLSLKCRCRCRVVSHPECDRCPLPCIPTLIGTPVKIGEGMLADFVSQTS 360

Db 301 VPCGKRIKFGKLSLKCRCRCRVVSHPECDRCPLPCIPTLIGTPVKIGEGMLADFVSQTS 360
Qy 361 MIPSIVVHCVNEIEQRLGTETGLYRISGCDRTVKELKEKFLRVKTVPLLSKVDDIHAICS 420
Db 361 MIPSIVVHCVNEIEQRLGTETGLYRISGCDRTVKELKEKFLRVKTVPLLSKVDDIHAICS 420
Qy 421 LKDFLRLNKEPLLTFRNLRAFMEAAEITDSDNSIAAMYQAVGELPOANRDTLAFMIHL 480
Db 421 LKDFLRLNKEPLLTFRNLRAFMEAAEITDSDNSIAAMYQAVGELPOANRDTLAFMIHL 480
Qy 481 ORVAQSPHTKMDVANLAKVFGPTTVAHAVPNPDVTHMSQDIKROPKVVVERLLSLPLEYWS 540
Db 481 ORVAQSPHTKMDVANLAKVFGPTTVAHAVPNPDVTHMSQDIKROPKVVVERLLSLPLEYWS 540
Qy 541 QFMVVEQENIDPLHVIENSNAFSTPQTDIKVSLGPGVTTPEHQLLKTSPSSSSLSQVRVS 600
Db 541 QFMVVEQENIDPLHVIENSNAFSTPQTDIKVSLGPGVTTPEHQLLKTSPSSSSLSQVRVS 600
Qy 601 TLTKNTPRFGSKSKSATNLGRQGNFFASPMLK 632
Db 601 TLTKNTPRFGSKSKSATNLGRQGNFFASPMLK 632

RESULT 5

US-10-756-149-5722
; Sequence 5722, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
; TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/756,149
; CURRENT FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5722
; LENGTH: 632
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-756-149-5722

Query Match 99.6%; Score 3230; DB 5; Length 632;
Best Local Similarity 99.7%; Pred. No. 3.6e-257;
Matches 630; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MDTMMLNVRNLFEOQLVRRVEILSEGNEVQFIQLAKDPEDFRKKWQRTDHELKGYKDLIMK 60
Db 1 MDTMMLNVRNLFEOQLVRRVEILSEGNEVQFIQLAKDPEDFRKKWQRTDHELKGYKDLIMK 60
Qy 61 AETERSALDVKLKHARNQVDVEIKRQRAEADCEKLEQIQLIREMLMCDTSGSIQJSEE 120
Db 61 AETERSALDVKLKHARNQVDVEIKRQRAEADCEKLEQIQLIREMLMCDTSGSIQJSEE 120
Qy 121 QKSALAFNLNRQSPSSNAGNKRSLTIDSGSILSDISFDKTDDESILWDSLSLVKTFKLKCR 180
Db 121 QKSALAFNLNRQSPSSNAGNKRSLTIDSGSILSDISFDKTDDESILWDSLSLVKTFKLKCR 180
Qy 181 EKRRSTSRQFVDPGPPGVKKTRSIGSAVDQGNESIVAKTTVTPVNDGPGPIEAVSTIETVP 240
Db 181 EKRRSTSRQFVDPGPPGVKKTRSIGSAVDQGNESIVAKTTVTPVNDGPGPIEAVSTIETVP 240
Qy 241 YWTRSRRTGTLOPWNSTLNSRQLEPRTETSDVGTQPSNGMRLHDFVSKTVIKPESC 300
Db 241 YWTRSRRTGTLOPWNSTLNSRQLEPRTETSDVGTQPSNGMRLHDFVSKTVIKPESC 300
Qy 301 VPCGKRIKFGKLSLKCRCRCRVVSHPECDRCPLPCIPTLIGTPVKIGEGMLADFVSQTS 360
Db 301 VPCGKRIKFGKLSLKCRCRCRVVSHPECDRCPLPCIPTLIGTPVKIGEGMLADFVSQTS 360
Qy 361 MIPSIVVHCVNEIEQRLGTETGLYRISGCDRTVKELKEKFLRVKTVPLLSKVDDIHAICS 420

Db 361 MIESIVHCVNEIEQRLTETGLYRISGCDRTVKELKEKFLRVKTVPLLSKVDDIIHAICS 420
Qy 421 LLKDFLRLNKEPLLTFRLNRAFMEEAAEITDDEDSIAAMYQAVGELPQANRDTLAFMLHL 480
Db 421 LLKDFLRLNKEPLLTFRLNRAFMEEAAEITDDEDSIAAMYQAVGELPQANRDTLAFMLHL 480
Qy 481 QRVASPHTKMDVANLAKVFGPTTIVAHAVNPDPVTMSQDIKQPKVVERLLSLPLEYWS 540
Db 481 QRVASPHTKMDVANLAKVFGPTTIVAHAVNPDPVTMLQDIKQPKVVERLLSLPLEYWS 540
Qy 541 QFMVQENIDPLHVIENSNAFSTPQTPDIKVSLLGVPVTPPEHQLLKTTPSSSSLSORVRS 600
Db 541 QFMVQENIDPLHVIENSNAFSTPQTPDIKVSLLGVPVTPPEHQLLKTTPSSSSLSORVRS 600
Qy 601 TLTNTPRFGSKSATNLGRQGNFFASPMK 632
Db 601 TLTNTPRFGSKSATNLGRQGNFFASPMK 632
RESULT 6
US-09-833-790-427
; Sequence 427, Application US/09833790
; Patent No. US20020068288A1
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Wang, Tongtong
; APPLICANT: Secrist, Heather
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Indirias, Carol Y.
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.512
; CURRENT APPLICATION NUMBER: US/09/833,790
; CURRENT FILING DATE: 2001-04-11
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 427
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-790-427

Query Match 90.0%; Score 2919; DB 3; Length 570;
Best Local Similarity 99.8%; Pred. No. 1.4e-231;
Matches 569; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 63 TERSALDVKLKHARNQVDVEIKRRQRAEADCEKLERQIQLIREMLMCDTSGSIQISEQK 122
Db 1 TERSALDVKLKHARNQVDVEIKRRQRAEADCEKLERQIQLIREMLMCDTSGSIQISEQK 60
Qy 123 SALAFLNRGQPSSSNAGNKKLSTIDSGSILSDISFDKTDDESIDWDSSSLVKTPLKKREK 182
Db 61 SALAFLNRGQPSSSNAGNKKLSTIDSGSILSDISFDKTDDESIDWDSSSLVKTPLKKREK 120
Qy 183 RRSRSRQFVDPGPPVKKTRSIGSAVDQGNESIVAKTTVTPNDGGPIEAVSTIETVPYW 242
Db 121 RRSRSRQFVDPGPPVKKTRSIGSAVDQGNESIVAKTTVTPNDGGPIEAVSTIETVPYW 180
Qy 243 TRSRRTKTGLQPNWNSDSTLNSRQLEPRTESTDVGTQPSNGMRLHDFVSKTVIKPESCPV 302
Db 181 TRSRRTKTGLQPNWNSDSTLNSRQLEPRTESTDVGTQPSNGMRLHDFVSKTVIKPESCPV 240
Qy 303 CGKRIKFGKLSKCRDCRVVSHPECDRCPLCPIPTLIGTPVKIGEGMLADFVSQISPMI 362
Db 241 CGKRIKFGKLSKCRDCRVVSHPECDRCPLCPIPTLIGTPVKIGEGMLADFVSQISPMI 300
Qy 363 PSIVHVCVNEIEQRLTETGLYRISGCDRTVKELKEKFLRVKTVPLLSKVDDIIHAICSLL 422
Db 301 PSIVHVCVNEIEQRLTETGLYRISGCDRTVKELKEKFLRVKTVPLLSKVDDIIHAICSLL 360
Qy 423 KDFLRLNKEPLLTFRLNRAFMEEAAEITDDEDSIAAMYQAVGELPQANRDTLAFMLHLQR 482

Db 361 KDFLRLNKEPLLTFRLNRAFMEEAAEITDDEDSIAAMYQAVGELPQANRDTLAFMLHLQR 420
Qy 483 VAQSPHTKMDVANLAKVFGPTTIVAHAVNPDPVTMSQDIKQPKVVERLLSLPLEYWSQF 542
Db 421 VAQSPHTKMDVANLAKVFGPTTIVAHAVNPDPVTMLQDIKQPKVVERLLSLPLEYWSQF 480
Qy 543 MMVEQENIDPLHVIENSNAFSTPQTPDIKVSLLGVPVTPPEHQLLKTTPSSSSLSORVSTL 602
Db 481 MMVEQENIDPLHVIENSNAFSTPQTPDIKVSLLGVPVTPPEHQLLKTTPSSSSLSORVSTL 540
Qy 603 TKNTPRFGSKSATNLGRQGNFFASPMK 632
Db 541 TKNTPRFGSKSATNLGRQGNFFASPMK 570
RESULT 7
US-09-881-736-4
; Sequence 4, Application US/09881736
; Patent No. US20020076785A1
; GENERAL INFORMATION:
; APPLICANT: Glotzer, Michael
; APPLICANT: Jantsch-Plunger, Verena
; APPLICANT: Romano, Alper
; APPLICANT: Mishima, Masanori
; APPLICANT: Kaitha, Susanne
; TITLE OF INVENTION: Cyk-4 polypeptides, DNA molecules encoding them and their use in
; FILE OF INVENTION: screening methods
; FILE REFERENCE: 0652.2260001/EKS/AES
; CURRENT APPLICATION NUMBER: US/09/881,736
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: EP 00 112 880.0
; PRIOR FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: EP 01 110 554.1
; PRIOR FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 60/241,231
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: To be determined
; PRIOR FILING DATE: 2001-06-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 628
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-881-736-4

Query Match 84.3%; Score 2734; DB 3; Length 628;
Best Local Similarity 84.4%; Pred. No. 3e-216;
Matches 534; Conservative 47; Mismatches 46; Indels 6; Gaps 3;
Qy 1 MDTMMLNVRNLFPEQLVRRVVEILSEGNE-VQFTQLAKDFEDFRKKWQRTDHELGKVDLLM 59
Db 1 MDTMMLNVRNLFPEQLVRRVVEILSEGNESTIEFTQVVKDFEDFRKKYQRTNQELEKPKDLLL 60
Qy 60 KAETRSALDVKLKHARNQVDVEIKRRQRAEADCEKLERQIQLIREMLMCDTSGSIQISE 119
Db 61 KAETRSALDVKLKHARNQVDVEIKRRQRAEADCEKLERQIQLIREMLMCDTSGSIQISE 120
Qy 120 EOKSALAFNLRGQPSSSNAGNKKLSTIDSGSILSDISFDKTDDESIDWDSSSLVKTPLKK 179
Db 121 EOKSALAFNLRGQPSSSNAGNKKLSTIDSGSILSDISFDKTDDESIDWDSSSLVKTPLKK 180
Qy 180 REKRSTRSRQFVDPGPPVKKTRSIGSAVDQGNESIVAKTTVTPNDGGPIEAVSTIETV 239
Db 181 REKRSTRSRQFVDPGPPVKKTRSIGSTVDQANESIVAKTTVTPSDGGPIEAVSTIETL 240
Qy 240 PWTSRRTKTGLQPNWNSDSTLNSRQLEPRTESTDVGTQPSNGMRLHDFVSKTVIKPES 299
Db 241 PSWTRSRGSGPLQPVNSDSALNSRPLEPRTDNLGTQNTGGMRLHDFVSKTVIKPES 300
Qy 300 CVPCKRIKFGKLSKCRDCRVVSHPECDRCPLCPIPTLIGTPVKIGEGMLADFVSQIS 359

Db 301 CVPCGKRIKFGKSLKDCRLVSHVPECDRCPLPPIPLVGTVPVKIGEGMLADVFVSQAS 360
Qy 360 PMPIGVVHVCNVEIQRGLTETGLYRISGCDRTVKELKEKFLRVKTVPLLSKVDDIHAIC 419
Db 361 PMPIGVVHVCNVEIQRGLTETGLYRISGCDRTVKELKEKFLRVKTVPLLSKVDDIHAIC 420
Qy 420 SLLKDFLNLKEPLLTFFLNRAFMFAAIBITDEDNSIAAMYQAVGELPOANRDTTLAFMLIH 479
Db 421 SLLKDFLNLKEPLLTFFLNRAFMFAAIBITDEDNSIAAMYQAVGELPOANRDTTLAFMLIH 480
Qy 480 LQVVAQSPHTKMDVANLAKVGPPTIVAHAVNPDPVMTSQDIKQPKVVERLLSLPLEYW 539
Db 481 LQVVAQSPHTKMDVANLAKVGPPTIVAHAVNPDPVMTSQDIKQPKVVERLLSLPLEYW 540
Qy 540 SQFMVVEQENIDPLHVIENSNAFSTPQTDIKVSLLGPTVTPPEHQLLKTSPSSSSLSQVR 599
Db 541 NQFMVVDQENIDS---QRGNGNSTPTPDVKVSLLGPTVTPPEHQLLKTSPSSSSLSQVR 599
Qy 600 STLTKNTPRFGSKSATNLGRQGNFFPASPMLK 632
Db 597 N-LSKSTPRFGNKSATNLGRQGNFFPASPMLK 628

RESULT 8

US-10-408-765A-1045
; Sequence 1045, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Bojin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1045
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1045

Query Match 36.4%; Score 1182; DB 4; Length 255;
Best Local Similarity 99.2%; Pred. No. 8.4e-89;
Matches 234; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 397 KEKFLRVKTVPLLSKVDDIHAICSLKDFLNLKEPLLTFFLNRAFMFAAIBITDEDNSIA 456
Db 20 KLEFLRVKTVPLLSKVDDIHAICSLKDFLNLKEPLLTFFLNRAFMFAAIBITDEDNSIA 79
Qy 457 AMYQAVGELPOANRDTTLAFMLIHQVVAQSPHTKMDVANLAKVGPPTIVAHAVNPDPVT 516
Db 80 AMYQAVGELPOANRDTTLAFMLIHQVVAQSPHTKMDVANLAKVGPPTIVAHAVNPDPVT 139
Qy 517 MSQDIKQPKVVERLLSLPLEYWQFMVVEQENIDPLHVIENSNAFSTPQTDIKVSLLG 576
Db 140 MQDIKQPKVVERLLSLPLEYWQFMVVEQENIDPLHVIENSNAFSTPQTDIKVSLLG 199
Qy 577 PVTTPPEHQLLKTSPSSSSLSQVRSTLTNTNTPRFGSKSATNLGRQGNFFPASPMLK 632
Db 200 PVTTPPEHQLLKTSPSSSSLSQVRSTLTNTNTPRFGSKSATNLGRQGNFFPASPMLK 255

RESULT 9

US-11-097-143-30960
; Sequence 30960, Application US/11097143
; Publication No. US20050208558A1

; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR FILING DATE: 2005-04-04
; PRIOR FILING DATE: 1999-10-05
; PRIOR FILING DATE: 1999-10-19
; PRIOR FILING DATE: 1999-10-19
; PRIOR FILING DATE: 1999-10-28
; PRIOR FILING DATE: 1999-11-12
; PRIOR FILING DATE: 2000-01-12
; PRIOR FILING DATE: 2000-02-24
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30960
; LENGTH: 625
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-30960

Query Match 26.6%; Score 864; DB 6; Length 625;
Best Local Similarity 35.1%; Pred. No. 5.9e-62;
Matches 228; Conservative 110; Mismatches 225; Indels 86; Gaps 21;
Qy 4 MMLNVRNLPQLVRRVEILSEGN-EVQFIQLAKDFEDFRKKWQRTDHELKGYKDLLMKA 62
Db 1 MALSALASFDLRLRCMQVLTDTGTPPEEFLEFLRMFEQYHEKACAGYAAETARIQNELDKSL 60
Qy 63 TERSALDVKLKHARNQVDVVEIKRQRAADCEKLEKLEKLEKLEKLEKLEKLEKLEKLEK 122
Db 61 TKMGDLEGKLFHARRIIDMEIKARRQAEHERDAMESKIMAVADLLRHERN---LNNETR 116
Qy 123 SALAFNLRGOPSSS-----NA--GNKELSTIDSSGSLSDISFDKT--DESILDWSSLVKT 174
Db 117 DKLAFLLHT-LPSSRRKRSKSLNAVREDKSYGDNSTGSLLSLSTHSEDDFLD-----VRT 170
Qy 175 FKLKREKRSTGRQV-----DGPPGPKVKKTR--SIGSAVD----- 209
Db 171 SK-SWREHRSPLKQNPSPVGNKRSRLSTGLNGSMSTTTTGTGSRSSVGIQVGHQTV 229
Qy 210 --QGNESIVAKTTVTVPNDG-GPIEAVSTIETVYVTRSRKKTGTLOPWNSSDSTLNSQL 266
Db 230 VQGAERFCATTKVTIPDQGGVIRAEFTIESLPVIAGNERIGDGLSSTPRSSVLKEATA 289
Qy 267 EPTETDSV-----GTP-QSNGMRLHDFVSKTVIKPESCVPCGKRIKFGKLSLKR 317
Db 290 PPLTPVNAMAPHVVAESGTFLOHRLRNHTFSQKTFLRGDNVCQCKRIRFGAVLR 349
Qy 318 DCRVSHPECDRCPLPPIPLVGTVPVKIGEGMLADVFVSQSPMIPSIHVHVCNVEIQR 376
Db 350 DCPVRCHIDCRYLLTTSVCPQV-TGTPYTKTWTGVTDFAPSIAPMIPALIVHVCNVEIQR 408
Qy 377 GLTETGLYRISGCDRTVKELKEKFLRVKTVPLLSKVDDIHAICSLKDFLNLKEPLLT 436
Db 409 GLTEVGLYRLSSSREYKALKEQFLRGKATPHLGN-TDIVVLCCKVDFLRSLEPT 467
Qy 437 RLNRAPFMAEABITDEDNSIAAMYQAVGELPOANRDTTLAFMLIHQVVAQSPHTKMDVANL 496
Db 468 SOWKDFANAVQNPDTKTAQDMLVKVSKQLPOANRDTTLAFMLIHQVVAQSPHTKMDVANL 527

; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

; FILE REFERENCE: 790CIE3/US

; CURRENT APPLICATION NUMBER: US/10/450,763

; CURRENT FILING DATE: 2003-06-11

; PRIOR FILING DATE: 2001-03-30

; PRIOR APPLICATION NUMBER: PCT/US01/08631

; PRIOR FILING DATE: 2001-03-30

; PRIOR APPLICATION NUMBER: 09/540,217

; PRIOR FILING DATE: 2000-03-31

; PRIOR APPLICATION NUMBER: 09/649,167

; PRIOR FILING DATE: 2000-08-23

; NUMBER OF SEQ ID NOS: 60736

; SOFTWARE: Custom

; SEQ ID NO 50263

; LENGTH: 1086

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: DOMAIN

; LOCATION: (354)..(379)

; OTHER INFORMATION: 7 kw REVERSE TRANSCRIPTASE RNA POLYMERASE domain identified

; OTHER INFORMATION: by eMATRIX, accession number DM00895E, p-value=3.667e-11, raw score

; OTHER INFORMATION: of 15.72

; FEATURE:

; NAME/KEY: DOMAIN

; LOCATION: (315)..(600)

; OTHER INFORMATION: Reverse transcriptase domain identified by Pfam, accession

; OTHER INFORMATION: name rvt, E-value=2.8e-64, Pfam score of 227.0

US-10-450-763-50263

Query Match 19.1%; Score 618; DB 5; Length 1086;

Best Local Similarity 46.9%; Pred. No. 2.8e-41;

Matches 153; Conservative 35; Mismatches 68; Indels 70; Gaps 11;

Qy 255 WNSTLNSRLQLEPRTEQTSVGTQSGMRLHDFVSKTVIKPSCVPCGKRIKFKLSL 314

Db 790 WIKD--LNVPRKTKTLEENLGNITQDIGMG-KDFMSKT---PKAMATKTKIDKWDLIQL 843

Qy 315 KCRDCRVVSHPECDRCPLCIPTLIGTPVKIG-----EGMLADFVSQTSMPISVWH 368

Db 844 KSFFC-----TAKETIRVNQPTWEKIFATYSSD-----KGLISR 880

Qy 369 CVNIEQ-----RGLTETGLY-----RISGCDR--TVKELKEK-FLRV 403

Db 881 IYNELKQIYKKTNPIKKTNDNRHFSKEDIYAAKKHMKKCSLPAIREMQIKTTMY 940

Qy 404 KTVPLL-----SKVDDIHAICSLDKDFLRLKEPLLTFLRLNAFMAAEITDEDN 453

Db 941 HLTPVRIAIKKSGNNSKVDDIHAICSLDKDFLRLKEPLLTFLRLNAFMAAEITDEDN 1000

Qy 454 SIAMYQAVGELPOANRDTLAFMLHLQORVAQSPHTKMDVANLAKVFGPTTIVAHAVNP 513

Db 1001 SISAMYQAVGELPOANRDTLVFLMIHLQORVAQSPHTKMDVANLAEVFGSTIVAHAVNP 1060

Qy 514 PVTMSQDIKQPKVVERLLSLPLEYW 539

Db 1061 PVTMLQDIKQPKVVERLPSLPLEYW 1086

RESULT 13

US-10-450-763-44317

; Sequence 44317, Application US/10450763

; Publication No. US20050196754A1

; GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc

; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

; FILE REFERENCE: 790CIE3/US

; CURRENT APPLICATION NUMBER: US/10/450,763

; CURRENT FILING DATE: 2003-06-11

; PRIOR APPLICATION NUMBER: PCT/US01/08631

; PRIOR FILING DATE: 2001-03-30

; PRIOR APPLICATION NUMBER: 09/540,217

; PRIOR FILING DATE: 2000-03-31

; PRIOR APPLICATION NUMBER: 09/649,167

; PRIOR FILING DATE: 2000-08-23

; NUMBER OF SEQ ID NOS: 60736

; SOFTWARE: Custom

; SEQ ID NO 44317

; LENGTH: 1139

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: DOMAIN

; LOCATION: (390)..(435)

; OTHER INFORMATION: kw TRANSCRIPTASE REVERSE II ORF2 domain identified by

; OTHER INFORMATION: eMATRIX, accession number DM01354N, p-value=1.000e-40, raw score

; OTHER INFORMATION: 13.17

US-10-450-763-44317

Query Match 19.1%; Score 618; DB 5; Length 1139;

Best Local Similarity 45.0%; Pred. No. 3e-41;

Matches 158; Conservative 39; Mismatches 70; Indels 84; Gaps 14;

Qy 242 WTSRRTGTQLPWNDSST-LNSR-----QLEPRTEQTSVGTQSGMRLH-----DF 289

Db 820 WLAICRKL-KLDPFLTAYTKINSRWIKDLNIREKT---IKTLEENLGIITQDIGMGKDF 874

Qy 290 VSKTVIKPSCVPCGKRIKFKLSLRCDCRVVSHPECDRCPLCIPTLIGTPVKIG-- 347

Db 875 MSKT---PKAMATKTKIDKWDLIQLKSFFC-----TAKETIRVNQ 913

Qy 348 -----EGMLADFVSQTSMPISVIVHCVNIEQ-----RGLTETGLY- 384

Db 914 PTEWEKIFATYSSD-----KGLISRINYELKQIYKKTNPIKKTNDNRHFSKEDIYA 968

Qy 385 ---RISGCDR--TVKELKEK-FLRVKTVPLL-----SKVDDIHAICSLDKDFLRL 428

Db 969 AKHMKKCSLPAIREMQIKTTMYHLTPVRIAIKKSGNNSKVDDIHAICSLDKDFLRL 1028

Qy 429 LKPEPLTFLRLNAFMAAEITDEDNSIAMYQAVGELPOANRDTLAFMLHLQORVAQSPH 488

Db 1029 FKEPLLTFLRLNAFMAAEITDEDNSIAMYQAVGELPOANRDTLVFLMIHLQORVAQSPY 1088

Qy 489 TKMDVANLAKVFGPTTIVAHAVNPDPVTMSQDIKQPKVVERLLSLPLEYW 539

Db 1089 TKMDVANLAEVFGSTIVAHAVNPDPVTMLQDIKQPKVVERLPSLPLEYW 1139

RESULT 14

US-09-881-736-6

; Sequence 6, Application US/09881736

; Patent No. US20020076785A1

; GENERAL INFORMATION:

; APPLICANT: Glotzer, Michael

; APPLICANT: Jantsch-Plunger, Verena

; APPLICANT: Romano, Alper

; APPLICANT: Mishima, Masanori

; APPLICANT: Kaitna, Susanne

; TITLE OF INVENTION: Cyk-4 polypeptides, DNA molecules encoding them and their use in

; FILE REFERENCE: 0652.2260001/EKS/AES

; CURRENT APPLICATION NUMBER: US/09/881,736

; CURRENT FILING DATE: 2001-06-18

; PRIOR APPLICATION NUMBER: EP 00 112 880.0

; PRIOR FILING DATE: 2000-06-19

; PRIOR APPLICATION NUMBER: EP 01 110 554.1

; PRIOR FILING DATE: 2001-04-30

; PRIOR APPLICATION NUMBER: 60/241,231

; PRIOR FILING DATE: 2000-10-18

; PRIOR APPLICATION NUMBER: To be determined

; PRIOR FILING DATE: 2001-06-13

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 6

; LENGTH: 681

; TYPE: PRT

; ORGANISM: Caenorhabditis elegans


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US-09-881-736-6
Query Match      16.7%; Score 541.5; DB 3; Length 681;
Best Local Similarity 25.9%; Pred. No. 2.8e-35;
Matches 180; Conservative 109; Mismatches 285; Indels 121; Gaps 22;

QY 7 NVNRLFEQLVRRVEILSEGNEVQFIQAKDFEFPRKW-----QRTDHELKGYKDLIM 59
DB 14 NSRHIFNMILNSORPQDINKGMFHLDIERLKLWKDSESKRLNADREAEALA 73
QY 60 KAETERSALVDKLKHARNVDVIEKRRORAEACEKLERIOILIREMLMCDTSGSLQSE 119
DB 74 KAKKULAMFIDVKTQKHRLMEENKALKJDLNVYETREKOLKAMKNGIFNS--LTK 131
QY 120 EOKSALAFNRGQSSNAGNKRSLTIDESGSLDISFDKTDSELDWD---SSLVKTFK 176
DB 132 EDRDPQFKLHE--PLVRTYSKRVQ--QRPHLMEDTQDDDDSEVDYDGTGSFEEVIH 186
QY 177 LKK-REKRSTS-----RQVDPGPPG-----PVKK 200
DB 187 LRNGREVRSSAAGNAGVGKRRSASAHATAAANSKRSRVMTATIDEEPNEGTPPKR 246
QY 201 TRSGSAVDGNGESIVAKTTVT-----VPNDGSP-----IEAVSTTETVP 240
DB 247 CRDGGSTPHQEMTTTTTTTTTIHNSRAQNDPPRVSLHRQLTRSLSCGSIPTSCDQTP 306
QY 241 YWTRSREKKTGTLPWNSDSTNSRQLEPRTEPDSVGTQPSNGGMRLHDFVSKTVIKPESC 300
DB 307 GQTTNNIGLWSSAILTKSLDITLTKRGTPAWNGTTR-DIAMRPHFTIEAGIKAMRKC 365
QY 301 VPGKRIKFKGLSLKCRDRCRVVSHPECDRCPLPCIP-----TLIGTPVKIGEGM 350
DB 366 DKCATALKLA-TSMKCRDCHQVHRSCCNKHLPCIPRPKTMTPKSALRGAKPGAGEFR 424
QY 351 LADPVSTQSPMPSIVVHCNEIEBQGLTETGLYRISGCDRTVKELKEFLRVKTVPLLS 410
DB 425 LQDCTSAKMPIPAVTHCVVLEARGLTQEGYRVPQVQRTVNVLLDE-LRSKTVPNVG 483
QY 411 KVDDIHAICSLDKDFLRNLKEPLLTFLRNLAFMEAEAI--TDEDNSTAAAMYQAVGELPQA 468
DB 484 -LHDVEVITDLKFLRDLKDLIPTRSQBELIVANLYSTDPDNGRLANRVICELPQA 542
QY 469 NRDTLAFMIHLQRV-AQSPTKMDVANLAKVFGPTIVAHAVPNPDVPMQO-----D 520
DB 543 NRDTLAYLFHWRKVIAQSSRNKNMCEAMARWAPAVMGH-----PVKOSQQAIGRD 596
QY 521 IKRQPKVVERLLSLPLEYWSQFMVVEQENIDPLHVIENSNAFSTPQTFD---IKVSLIG 576
DB 597 ATDCHRAWTALFEFDDVYWRFGTSA-----VSMASNQIETARHODNFALCDRSILG 649
QY 577 PVTTPEHQLLKTSSSSLSQSRVSRSTLTKNTPRFGS 611
DB 650 PVTT-----SPATPLARSANATRARGAHLIGS 677

RESULT 15
US-11-097-143-4533
; Sequence 4533, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
;

; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4533
; LENGTH: 384
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-4533

Query Match      14.7%; Score 477; DB 6; Length 384;
Best Local Similarity 40.7%; Pred. No. 2.4e-30;
Matches 110; Conservative 44; Mismatches 102; Indels 14; Gaps 6;

QY 279 QSNGG-MRLHDFVSKT-VIKPESCVPQGRKIRKFGKLSLKRCDCRVVSHPECDRCPLPCI 336
DB 78 QSHSGLLREHNFKISYYVNVGNCVHCRCRIEFAMASLECRACPLRCHIGCCQRLTVNCI 137
QY 337 P-TLIGTPVKIGEGMLADPVSTQSPMPSIVVHCNEIEBQGLTETGLYRISGCDRTVKE 395
DB 138 PQPQIGTK----RGCLSDYAPRVAPMPALIVHCVTEIEARGLQGBGLYRVSSTREKCKR 193
QY 396 LKEKEFLRVKTVPLLSKVDDIHAICSLDKDFLRNLKEPLLTFLRNLAFMEAEAITDEDSI 455
DB 194 LRRKLIRGKSTPHLGN-KDTHTLCCCVKDFLRQLVHPLIPIYHRDRDFEATRHEDRLAVE 252
QY 456 AAMYQAVGSLPOANRDTLAFMIHLQRVAQSPTKMDVANLAKVFGPTIVAHAVPNPDV 515
DB 253 MAVYLAVLELHQHRDRTLAYLMHLWQKIAESPAVMTVNNLAVIFAPTILFG-----DLD 306
QY 516 TMSQDIKQPKVVERLLSLPLEYWSQFMV 545
DB 307 LITLENVVTTWQVRLKVLILLMPAGFWSQFLEV 336

Search completed: August 9, 2006, 16:37:36
Job time : 187 secs
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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 9, 2006, 16:34:40 ; Search time 35 Seconds
(without alignments)
1215.463 Million cell updates/sec

Title: US-09-881-736A-2

Perfect score: 3243

Sequence: 1 MDTMLNVRNLFQVRRVE.....SKSATNLGRQGNFFASPMILK 632

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 239914 seqs, 67312017 residues

Total number of hits satisfying chosen parameters: 239914

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA New:

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	327	10.1	1169	6	US-10-449-902-41184
2	247.5	7.6	617	7	US-11-293-697-4817
3	240	7.4	1181	6	US-10-449-902-41178
4	229.5	7.1	655	7	US-11-285-052-2
5	229.5	7.1	655	7	US-11-265-052-23
6	229.5	7.1	655	7	US-11-265-065-2
7	229.5	7.1	655	7	US-11-265-065-23
8	229	7.1	1126	7	US-11-293-697-3665
9	203.5	6.3	286	7	US-11-293-697-3026
10	194	6.0	731	6	US-10-480-962-13
11	194	6.0	731	7	US-11-293-697-4126
12	176.5	5.4	727	6	US-10-480-962-14
13	171	5.3	1075	6	US-10-322-836-48
14	156	4.8	376	7	US-11-056-355B-49975
15	156	4.8	376	7	US-11-056-355B-50883
16	154	4.7	369	6	US-10-449-902-35324
17	154	4.7	369	6	US-10-449-902-46157
18	147	4.5	919	7	US-11-251-465-31
19	144.5	4.5	369	7	US-11-056-355B-69312
20	140.5	4.3	369	6	US-10-953-349-15280
21	140.5	4.3	369	6	US-11-056-355B-59816
22	128.5	4.0	667	6	US-10-471-571A-1414
23	128	3.9	371	7	US-11-056-355B-8588
24	127.5	3.9	1354	7	US-11-270-653-1
25	127	3.9	1205	7	US-11-293-697-2967

ALIGNMENTS

RESULT 1

US-10-449-902-41184
; Sequence 41184, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41184
; LENGTH: 1169
; TYPE: PRT
; ORGANISM: Oryza sativa
; US-10-449-902-41184

Query Match 10.1%; Score 327; DB 6; Length 1169;
Best Local Similarity 23.7%; Pred. No. 2.6e-13;
Matches 137; Conservative 89; Mismatches 239; Indels 114; Gaps 21;
Qy 9 RNLFQVRRVEILSEGVQFTQLAKDFDKKKQWTDHELGKY---KDLMKKAETER 65
Db 608 RLAEQALKATANSEKROQE--QLERSQDVKASLKGMRDLAKLTVERDLTVAEVAEL 665
Qy 66 SALD-----VKLKHARNQVDV-----EIKRQRAEADCEKLERQIQ 101
Db 666 MALQDGAAGPSSVLSPPNMASTSTSDAVITONLATRLSVKNRYRKEID-----ELT 719
Qy 102 LIREMLCMTSGSIQLSEOKSALAFINRGQPSSSNAGNKRISTIDESGILSDISPDKT 161
Db 720 MERDSL-----IEIEELKQSKELFEAAQ---SLNAKNEELNVLGQLNKLELAQSR 771
Qy 162 DE-----SLDWDSSLVK-----TFKLKREKRRTSRQ---FVDGPPGPFVKKRSIGS 206
Db 772 DQLPPLPTPRDLASATKSSGGFSGSRHKQLHKHTAHNASISSDAPPAGYDVSVDT 831
Qy 207 AVDQGNESIVAKTIVTPNDGGPIEAVSTIETVYVTRSRRTGTGTLPWNSDSTLN---- 262
Db 832 AVQQ-----VIQP-----GKIEPAPVV-----KPKMKMKPKLSETTRNNVPP 868

Sequence 44450, A
Sequence 1, Appli
Sequence 8779, Ap
Sequence 3533, Ap
Sequence 15, Appl
Sequence 51958, A
Sequence 41204, A
Sequence 8, Appli
Sequence 32, Appl
Sequence 22, Appl
Sequence 10, Appl
Sequence 10212, A
Sequence 10211, A
Sequence 3734, Ap
Sequence 84765, A
Sequence 84764, A
Sequence 84763, A
Sequence 41600, A
Sequence 66, Appl

26 126.5 3.9 608 6 US-10-449-902-44450
27 124 3.8 22152 6 US-10-544-944-1
28 123 3.8 1251 6 US-10-953-349-8779
29 122 3.8 209 7 US-11-293-697-3533
30 121 3.7 1087 6 US-10-486-020-15
31 120.5 3.7 494 6 US-10-449-902-51958
32 120 3.7 1045 6 US-10-449-902-41204
33 120 3.7 1084 7 US-11-251-643-8
34 119.5 3.7 1328 6 US-10-504-973-32
35 118.5 3.7 414 7 US-11-259-950-8
36 118 3.6 720 7 US-11-354-079-22
37 117.5 3.6 422 7 US-11-259-950-10
38 117 3.6 548 6 US-10-953-349-10212
39 117 3.6 574 6 US-10-953-349-10211
40 116.5 3.6 783 7 US-11-293-697-3734
41 116 3.6 747 7 US-11-056-355B-84765
42 116 3.6 865 7 US-11-056-355B-84764
43 116 3.6 890 7 US-11-056-355B-84763
44 115.5 3.6 763 6 US-10-449-902-41600
45 114.5 3.5 423 7 US-11-259-950-66

QY 263 SRQLEPRTESTDVG--TPQSNCG-----MRLHDFVSKTVIKPESVPCGKEI 307
Db 869 AGQVPVPKGGAGLAAPASGSGTSMTRATSHDVVREHLFPQFVNLRTTRCFACQKMN 928
QY 308 KFGKLSLKCRDCRWSHPECDRCPLCPTLITGTPVKIGEG-----MLADFVSQTS 359
Db 929 -WQSEMRCACTQVCHSRCLQSLPVCNQPYTRPDESVDNAGPMSFGESLVEQAAHEG 987
QY 360 PMTPIVHVCHVNBIEQRGLTETGLYRISGCDRTVKELKEKFLRVKTVPL--LSKVDDIHA 417
Db 988 RDVPLIVEKCIQAVEAFGMDYEGYRKSGTSQLKVIITQLFERGNAPFLEDTRDFNDVSA 1047
QY 418 ICSLLKDFLNLKEPLITFLRLNRAFMEAAEITDENSII--AAMYQAVGELPOANRDTLAF 475
Db 1048 ITSVLKNYFRELPTLLTFLYDELIRLVESKQGDAGAKQEKELVTRLPQRHFCTLOH 1107
QY 476 LMIHLQORVAQ--SPHTKMDVANLAKVGPPTIVAHAVNPDP 513
Db 1108 LVHLRVQERSVDNRNARNLGVFGPTLMRSADFSQE 1146

RESULT 2

US-11-293-697-4817
; Sequence 4817, Application US/11293697
; Publication No. US20060105376A1

; GENERAL INFORMATION:

; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4817
; LENGTH: 617
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-4817

Query Match 7.6%; Score 247.5; DB 7; Length 617;

Best Local Similarity 29.4%; Pred. No. 1.8e-08; Indels 25; Gaps 9;
Matches 83; Conservative 45; Mismatches 129;

QY 361 MIPSIYVHCVNEIEQRLTETGLYRISGCDRTVKELKEKFLRVKTVPLLSKVDDIHAICS 420
Db 56 LAPMLVEQCVDFFRQRLKEEGLFRLPGQANLVKELQDAF--DCGEKPSFDSNTDVHTVAS 114
QY 421 LLKDFLRLNKEPLITFLRLNRAFMEAAEII--TDEDSIAAMYQAVGELPOANRDTLAFMI 478
Db 115 LLKLYLRELPEVPIYAKVEDFLSCAKLLSKEEAGVKELAKQVKSPLPVVYNNLLKYICR 174
QY 479 HLQRV--AQSPHTKMDVANLAKVGPPTIVAHAVNPDPVTMSQDIKEQPKVVERLLSPLLE 537
Db 175 FLDEVSQYGVNKKVQNQLATVFGPNILRPKV--EDPLT----IMEGTVVVQQLMSVMIS 228
QY 538 YWQFMMVEQE--NIDPLHVIENSNATFSTPTDPIKVSLLGPTVTPHQLLTKPSSSLSS- 595
Db 229 KHDCLPDKDELQSKQDQGVSNNEIQ-----KKATWGQLQNKNNYTKDSPRQCSW 281
QY 596 -----QVRSTLTNKTNR--FGSKSKSATNLGRGNFFASPM 631
Db 282 DKSESPORSSMNGSPALSGSKTNSPKNSVHKLVDVSRSPPL 323

RESULT 3

US-10-449-902-41178
; Sequence 41178, Application US/10449902
; Publication No. US20060123505A1

; GENERAL INFORMATION:

; APPLICANT: National Institute of Agrobiological Sciences.

; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.

; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF

; FILE REFERENCE: MOA-A0205Y1-US

; CURRENT APPLICATION NUMBER: US/10/449,902

; CURRENT FILING DATE: 2003-05-29

; PRIOR APPLICATION NUMBER: JP 2002-203269

; PRIOR FILING DATE: 2002-05-30

; PRIOR APPLICATION NUMBER: JP 2002-383870

; PRIOR FILING DATE: 2002-12-11

; NUMBER OF SEQ ID NOS: 56791

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 41178

; LENGTH: 1181

; TYPE: PRT

; ORGANISM: Oryza sativa

US-10-449-902-41178

Query Match 7.4%; Score 240; DB 6; Length 1181;

Best Local Similarity 24.9%; Pred. No. 1.3e-07;
Matches 119; Conservative 58; Mismatches 173; Indels 128; Gaps 21;

QY 113 GSIQLSEEQKSALAFNLNRGQPSSSNAG-----NKRSLTIDESGILSDISPD 159

Db 612 GSNIRDAQ-----IGRQKSTASSEDENAYRHAFLILEKREGMPDEPAHIAHVLC 665

QY 160 KTDESL-DWDSLVKTF-----KLRKREKRTSRQF 190

Db 666 ESDEERDDVDVLVRAIAELDGVSLDDMPASPTQMSQMSLSQQATTGREALGSNAR--F 724

QY 191 VDG--PPGPVKTRSIGSAVDQ--GNESIVAK--TTVTVPNDGGPIEAVSTIEIVPYWTRSR 246

Db 725 PDSAFSPSADKAGROFGGDAGQDGSNRVAARNWSVDSTATGKPVGSTP-----GSSL 776

QY 247 RKTGTLQPNWSDSTLNSRQLERPTETDSVGTGTPQSGNGMRLHDFV-----SKTV 294

Db 777 PQSASYRSFN-----EPR-----SPVSSRGADLYDAPGSPGRNEPLNRKTS 819

QY 295 IK-PESCVPCGKRIKFG-----KLSLKCR-----DCRVVSHPECDRCPLCPTLTIG 341

Db 820 ISGPLNGAPIAGYKFGAKDDMGDPDSKKDDKKRFQGFAGFGSKDKHNRPRP-----VFG 875

QY 342 TPV-----KIGEGMLADFVSQTSPIVSVHVCVNELEQR--GLTETGLYRISGCDRTV 393

Db 876 VPLAESIAISSIHEGL-----ALPSVVYRCIEYLEKKNAPFMEEGIYRLSGSSAVI 925

QY 394 KELKEKFLRVKTVPLLSKVD--DIHAICSLKDFLRLNKEPLITFLRLNRAFMEAAEITDE 451

Db 926 KNLKDRFNMEGDVLDTENQYDDPHAIAGLLKTFRLPSTVLTRELHMDFRINELQDR 985

QY 452 DNSIAAMYQAVGELPOANRDTLAFMIHLQORVAQ--SPHTKMDVANLAKVFGPTIVAH 508

Db 986 VERVNELGRVLSQLPLANYSLRLTCLSHLIKIEHSDVNKMTMRNVGVFSPTLAIGA 1043

RESULT 4

US-11-265-052-2

; Sequence 2, Application US/11265052

; Publication No. US20060104982A1

; GENERAL INFORMATION:

; APPLICANT: University of Texas, Board of Regents

; TITLE OF INVENTION: THERAPIES FOR SEIZURE DISORDERS USING RLIP76

; FILE REFERENCE: 124263-1038

; CURRENT APPLICATION NUMBER: US/11/265,052

; CURRENT FILING DATE: 2005-11-02

; PRIOR APPLICATION NUMBER: 10/714,506

; PRIOR FILING DATE: 2003-11-13

; PRIOR APPLICATION NUMBER: 10/713,578

; PRIOR FILING DATE: 2003-11-13

; PRIOR APPLICATION NUMBER: 60/425,917

; PRIOR FILING DATE: 2002-11-13

; PRIOR APPLICATION NUMBER: 60/425,814

QY 350 MLADFVSQT-----SPMIPSIIVHCVNEIQRGILTETGLYRISGCDRTVVKELKEKFLRVKT 405
Db 194 -LADAVERTNMYDGLRLPAVFRICIDYVEKYGMKCEGIYRVSGIKSVKDELKAAAYDRSS 252
QY 406 VPLLSKVDDI--HAICSLKDFLNLKEPLLTPFLNRAFMEAAEITDEDNSTAAAMYQAVG 463
Db 253 -----TNLEDYEPNTVASLLKQYLRDLDPENLLTKELMPREEACGRTTETEKVQEFORLLK 308
QY 464 ELPOANDTLAFMLIHLQRY-AQSPHTKMDVANLAKVFGPTI 504
Db 309 ELPECNVLLISWLIVHMDHVIKAELETKNQIQNISIVLSPTV 350

RESULT 7
US-11-265-065-23
; Sequence 23, Application US/11265065
; Publication No. US20060104983A1
; GENERAL INFORMATION:
; APPLICANT: University of Texas, Board of Regents
; TITLE OF INVENTION: THERAPIES FOR THE REGULATION OF INSULIN AND GLUCOSE USING RLIP76
; FILE REFERENCE: 124263-1039
; CURRENT APPLICATION NUMBER: US/11/265,065
; CURRENT FILING DATE: 2005-11-02
; PRIOR APPLICATION NUMBER: 10/714,506
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 10/713,578
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,917
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 60/425,814
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23
; LENGTH: 655
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-265-065-23

Query Match 7.1%; Score 229.5; DB 7; Length 655;
Best Local Similarity 22.9%; Pred. No. 2.9e-07;
Matches 92; Conservative 69; Mismatches 146; Indels 95; Gaps 15;

QY 118 SEBQKSAALP---LNRQPSSSNAGNRLSTIDESGILSDISFDTKTDSDLDWDSLVKT 174
Db 29 SSEEISPTKPPGLYRTGERSPPH-----DILHEPPDVVSD---DEKDHG-----KKK 72
QY 175 FKLKKEKRSTSRQFVGGPPG-----PVKKTISGSAYDOGNESIVAKTIVTVPNDDGP 229
Db 73 GKFKKKEKRTGEGYAAPQEDSSGDEAESPSKMKRSKGIHVFK-----113
QY 230 IEAVSTIETVPYTRSRKRTGTLQPNWSDSTLNSRQLEPRTESTDVSGTTPQSNNGMRLHDF 289
Db 114 -----KPSFSKKEK-----DPKIKKPKKEKHKEK-HKEKHKEKSKDL 154
QY 290 VSKTVTKPESVCPGKRIKFGKLSLRCRDRVVSHPECDRCPLCPIPTLIGTPVKIGSG 349
Db 155 TAADVVK-----QWKEKKKKKKPKQIEPEV-PQIDVPLNKPFGIP-----193
QY 350 MLADFVSQT-----SPMIPSIIVHCVNEIQRGILTETGLYRISGCDRTVVKELKEKFLRVKT 405
Db 194 -LADAVERTNMYDGLRLPAVFRICIDYVEKYGMKCEGIYRVSGIKSVKDELKAAAYDRSS 252
QY 406 VPLLSKVDDI--HAICSLKDFLNLKEPLLTPFLNRAFMEAAEITDEDNSTAAAMYQAVG 463
Db 253 -----TNLEDYEPNTVASLLKQYLRDLDPENLLTKELMPREEACGRTTETEKVQEFORLLK 308
QY 464 ELPOANDTLAFMLIHLQRY-AQSPHTKMDVANLAKVFGPTI 504
Db 309 ELPECNVLLISWLIVHMDHVIKAELETKNQIQNISIVLSPTV 350

RESULT 8

US-11-293-697-3665
; Sequence 3665, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3665
; LENGTH: 1126
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-3665

Query Match 7.1%; Score 229; DB 7; Length 1126;
Best Local Similarity 27.6%; Pred. No. 6.5e-07;
Matches 80; Conservative 54; Mismatches 130; Indels 26; Gaps 10;

QY 351 LADFVSQTSMPISIVHCVNEIQRGLTETGLYRISGCDRTVVKELKEKFLRVKTVPLLS 410
Db 317 LGEHLSNSGQDPVQLRCCSEFIEAHGVVD-GIYRLSGVSSNIQLRHEF-DSERIPELS 374
QY 411 K---VDDIHAICSLKDFLNLKEPLLTPFLNRAFMEAAEITDEDNSTAAAMYQAVGELPO 467
Db 375 GPAFIQLDIHSVSSLCXYFRELPNLLTYQLYGFSEAMSVPGEERLVRVHDVIOQLPP 434
QY 468 ANRDTLAFMLIHLQRYAQ-SPHTKMDVANLAKVFGPTIVAHAVPNPDPVTMS-----QDI 521
Db 435 PHRYTLEYLLRHLARMARHSANTSMMHARNLATVWAPNLLRSM--ELESYMGGAAPREV 492
QY 522 KROPKVVVERLLS-LPLEYWSQFMVYEQENIDP---LHVINSNAFSTPOT-----PDIK 571
Db 493 RVQSVVVEFLTHVDVLFSDTF---TSAGLDPAGCLLPKPKSLAGSCDSTLLTLEEAQ 549
QY 572 VSLLGVTTPHEQLLKTPTSSLSQRVSRSTLTPTKNTPRFGSKSKSATNLGR 621
Db 550 ARTQGRLGTTPTTEPTTPKAPASPAERKKGEGEKQKPGSSWKTPFALGR 599

RESULT 9

US-11-293-697-3026
; Sequence 3026, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3026
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-3026

Query Match 6.3%; Score 203.5; DB 7; Length 286;
Best Local Similarity 26.4%; Pred. No. 4.6e-06;
Matches 73; Conservative 46; Mismatches 84; Indels 73; Gaps 10;

QY 414 DIHAICSLKDFLNLKEPLLTPFLNRAFMEAAEITDEDNSTAAAMYQAVGELPOANRDTL 473
Db 18 EIKTTISALKTYLRMLPGFLMMYQFQSFKAQKLENOESRVSEIHSLVHRLPEKNRML 77

Qy 474 AFLMIHLQVQAQS-PHTKMDVANLAKVFGPTIVAHAVNPDPVTMSODIKRQKVVVERLL 532
Db 78 QLLANHLANVANNHKNQMLTAVNLGVFGPTLLR---PQETVAIAINDIKFQNVIEILI 134
Qy 533 -----SLPLEYWSQPMWVEQENID-----PL-----HVIENSNAFSTPQTPD 569
Db 135 ENHEKIFNTVDMPLTN-AQLHLRKKSSDSKPPSCSERPLTLPHTVOSTE--KQBORNS 191
Qy 570 IKVSLGLGVTTPPEHQLLKTSSSLSQRVST-----SATNLGRQGN 624
Db 192 IINSLSVSNPNISILN--SSSSLOPNMNSDDPD LAVKPTRNSLPNPSPTSPSPS 249
Qy 606 TPRFGSKSK-----SATNLGRQGN 624
Db 250 WPMFSAFSSPMTSTSSDLSRLITWSSNRGPQON 285

RESULT 10
US-10-480-962-13
; Sequence 13, Application US/10480962
; Publication No. US20060115813A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Junming; EMERLING, Brooke M.;
; APPLICANT: TANG, Y. Tom; BAUGHN, Mariah R.;
; APPLICANT: LEE, Ernestine A.; RAMKOMAR, Jayalaxmi;
; APPLICANT: YUE, Henry; GRIFFIN, Jennifer A.;
; APPLICANT: CHAWLA, Narinder K.; TRAN, Bao
; APPLICANT: NGUYEN, Dannel B.; KHAN, Farrah A.;
; APPLICANT: GANDHI, Ameena R.; HAPALIA, April J.A.;
; APPLICANT: SWARNAKER, Anita; GURURAJAN, Rajagopal;
; APPLICANT: POLICKY, Jennifer L.; YAO, Monique G.;
; APPLICANT: WARREN, Bridget A.; GRETZEN, Kimberly J.;
; APPLICANT: ELIOTT, Vicki S.; LEE, Soo Yeun;
; APPLICANT: SANTANWALA, Bharati; HONCHELL, Cynthia D.;
; APPLICANT: FORSYTHE, Ian J.; GORVAD, Ann E.;
; APPLICANT: RICHARDSON, Thomas W.; LEE, Sally;
; APPLICANT: BARROSO, Ines
; TITLE OF INVENTION: INTRACELLULAR SIGNALING MOLECULES
; FILE REFERENCE: PP-1002 USN
; CURRENT APPLICATION NUMBER: US/10/480,962
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/US02/17955
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/297,010
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/298,706
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/299,998
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: US 60/300,377
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,871
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/303,349
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: US 60/303,403
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US 60/351,927
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PERL Program
; SEQ ID NO 13
; LENGTH: 731
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID NO: 2655990CD1

US-10-480-962-13
Query Match 6.0%; Score 194; DB 6; Length 731;
Best Local Similarity 22.1%; Pred. No. 7e-05;
Matches 97; Conservative 78; Mismatches 154; Indels 110; Gaps 19;

Qy 256 NSDSTLNSROLEPRTETDTSVGTQSGNGMRLHDFVSKTVIKPESC--VPCGKRIKFGKLS 313
Db 8 NASKTLNANNMETLIEC-----QSEGDIKEHPLLASCESESDICQLIEVKRKK----- 56
Qy 314 LKCRDCRVVSHPECRRD-CPLPCIPITLIGTPVKIGMGLAD-----FVSQTSMPISIVVH 368
Db 57 -----VLSWPFIMRLSPASDFSGALETDLK---ASLFDQPLSICGSDSLPRIQD 106
Qy 369 CVNIEIQRGLTETGLYRISGCDRTVRELKEKF-----LRVKTVPLLSKVDDIHAICSLLK 423
Db 107 ILTILCLKGPSTEGIFRRAANEKARKEELNSGDAVDLERLP-----VHLLAVVFK 159
Qy 424 DFLRNKPELLTFLRNAPFMAEAITDEDSIAAMYQAVGELPOANDTLAFLMIHLQV 483
Db 160 DFLRSIPRKLSSDLFEWMGALEMODEEDRIEALKQVADKLPRLNLLKHLVYVHLI 219
Qy 484 AQ-SPHYKMDVANLAKVFGPTIVAHAVNPDPVTM--SQDIKQPK-VVERLLSLPLEYW 539
Db 220 SKNSEVNRMDSSNLATCIGENML--TLENDQSLSFEAQKDLNNKVKTLVFEFLDNCFEIF 277
Qy 540 SQFMV-----EQENIDPLHVIENSNAFSTPQTPDIKVSLLGPVTTPEHQ----- 584
Db 278 GENIPVHSSITSDSLEHTDSSDVSTLONDSAYDS--NDPVESNSSSGISPSRQPOVPM 336
Qy 585 -----LTKT-----PSSS--LSQRV-RST 601
Db 337 ATAAGLDSAGPDAREVSPPIVSTVARLKSLSAQPDRRYSESPMSSQCSLESRTVNTQ 396
Qy 602 LTKN-----TPRFGSKSKS 615
Db 397 LTKSEGDFFPVPRVGSRLS 415
RESULT 11
US-11-293-697-4126
; Sequence 4126, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cdna
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4126
; LENGTH: 731
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-4126
Query Match 6.0%; Score 194; DB 7; Length 731;
Best Local Similarity 22.1%; Pred. No. 7e-05;
Matches 97; Conservative 78; Mismatches 154; Indels 110; Gaps 19;

Qy 256 NSDSTLNSROLEPRTETDTSVGTQSGNGMRLHDFVSKTVIKPESC--VPCGKRIKFGKLS 313
Db 8 NASKTLNANNMETLIEC-----QSEGDIKEHPLLASCESESDICQLIEVKRKK----- 56
Qy 314 LKCRDCRVVSHPECRRD-CPLPCIPITLIGTPVKIGMGLAD-----FVSQTSMPISIVVH 368
Db 57 -----VLSWPFIMRLSPASDFSGALETDLK---ASLFDQPLSICGSDSLPRIQD 106
Qy 369 CVNIEIQRGLTETGLYRISGCDRTVRELKEKF-----LRVKTVPLLSKVDDIHAICSLLK 423
Db 107 ILTILCLKGPSTEGIFRRAANEKARKEELNSGDAVDLERLP-----VHLLAVVFK 159
Qy 424 DFLRNKPELLTFLRNAPFMAEAITDEDSIAAMYQAVGELPOANDTLAFLMIHLQV 483
Db 160 DFLRSIPRKLSSDLFEWMGALEMODEEDRIEALKQVADKLPRLNLLKHLVYVHLI 219

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